

SEARCH REQUEST FORM

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51690

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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Type of Search		Vendors and cost where applicable
Searcher <u>Toby Fort</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # <u>308-354</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbi _____
Date Searcher Picked Up <u>9/26</u>	Bibliographic _____	Dr. Link _____
Date Completed <u>9/28</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time <u>10</u>	Fulltext _____	Sequence Systems <u>CS</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time <u>10</u>	Other _____	Other (specify) _____

Art : 5/2000

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 21.33 Seconds
(without alignments)
375.170 Million cell updates/sec

Title: US-09-662-783-4

Perfect score: 737

Sequence: 1 MYLTPRYGRSVHDKSKV.....DIQLDHHRCDCICSSRPPR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0601.*
- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
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 - 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
 - 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
 - 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
 - 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
 - 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
5 - 1	737	100.0	322	21	AA1971129 Human Platelet Der
2	737	100.0	370	21	AB48653 Human growth facto
3	737	100.0	370	21	AA196864 SEQ. ID. 37 from W
4 - 4	737	100.0	370	21	AA1971130 Human Platelet Der
5	737	100.0	370	22	AB60888 Human VEGF-G prote
6	713	96.7	200	21	AA1971128 Human Platelet Der
7	686	93.1	370	21	AB48663 Mouse growth facto
8	681	92.4	370	22	AB60895 Human VEGF-G prote
9	380	51.6	66	21	AA1971132 Human Platelet Der
10	330	44.8	374	21	AB10639 Human VEGF-X prote
11	328.5	44.6	149	21	AB10642 Human VEGF-X PDGF-

12	328.5	44.6	318	21	AA194558 A fragment of plat
13	328.5	44.6	339	21	AB58438 Lung cancer associ
14	328.5	44.6	345	20	AA193679 Human VEGF-E prote
15	328.5	44.6	343	20	AA191766 Human PRO200 prote
16	328.5	44.6	345	20	AA190023 Human vascular end
17	328.5	44.6	345	21	AB48657 Human zvegfg3, SEQ
18	328.5	44.6	345	21	AB24250 Human platelet-der
19	328.5	44.6	345	21	AB44322 Human PRO200 (UNQ1
20	328.5	44.6	345	21	AB10633 Human RACE generat
21	328.5	44.6	345	21	AB10634 Human VEGF-X homol
22	328.5	44.6	345	21	AB10635 Human VEGF-X prote
23	328.5	44.6	345	21	AB10636 Human VEGF-X prote
24	328.5	44.6	345	21	AB10644 Human 990126veg p
25	328.5	44.6	345	21	AB10650 Human VEGF-X prote
26	328.5	44.6	345	21	AB10651 Human VEGF-X prote
27	328.5	44.6	345	21	AB19578 Human PRO200 (vasc
28	328.5	44.6	345	21	AB33414 Human PRO200 prote
29	328.5	44.6	345	21	AB24412 Human PRO713 prote
30	328.5	44.6	345	21	AB01419 Human TANGO 128.
31	328.5	44.6	345	21	AB03003 Human growth facto
32	328.5	44.6	345	21	AA196858 Human growth facto
33	328.5	44.6	345	21	AA194557 Amino acid sequenc
34	328.5	44.6	345	21	AA19285 Bone morphogenic p
35	328.5	44.6	345	22	AB50980 Human PRO200 prote
36	328.5	44.6	345	22	AB49895 Human PRO200 prote
37	328.5	44.6	345	22	AB53074 Human angiogenesis
38	324.5	44.0	345	21	AB48658 Mouse zvegfg3, SEQ
39	324.5	44.0	345	21	AA196861 Murine vascular en
40	324.5	44.0	345	21	AA194559 A murine platelet-
41	318.5	43.2	354	21	AB10640 Human VEGF-X prote
42	318.5	43.2	354	21	AB10641 Human VEGF-X prote
43	308.5	41.9	113	21	AB10631 Human VEGF-X prote
44	308.5	41.9	113	21	AB10632 Human VEGF-X prote
45	292	39.6	227	21	AB10637 Human VEGF-X prote

ALIGNMENTS

RESULT 1

AA1971129	AA1971129 standard; peptide; 322 AA.
ID	AA1971129 standard; peptide; 322 AA.
XX	
AC	AA1971129;
XX	
DF	08-SEP-2000 (first entry)
XX	
DE	Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX	
KW	Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW	VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW	proliferative; activator; proliferation; differentiation; motility;
KW	growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW	atherosclerosis; wound; metastasis.
XX	
OS	Homo sapiens.
XX	
PN	WO200027879-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1999; 99WO-US26462.
XX	
PR	10-NOV-1998; 98US-0107852.
PR	28-DEC-1998; 98US-0113997.
PR	26-AUG-1999; 99US-0150604.
PR	04-OCT-1999; 99US-0157108.
PR	05-OCT-1999; 99US-0157756.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	
PI	Eriksson U, Aase K, Ponten A, Lee X, Utela M, Alitalo K;

PI Oestman A, Heldin C;
XX
DR WPI: 2000-376495/32.
DR N-PSDB; AAD00737.
XX
XX Novel polynucleotides encoding a novel growth factor of cells
PT expressing a platelet-derived growth factor, useful for diagnostic and
PT therapeutic applications, e.g. concerning cancer -
XX
XX Claim 25; Fig 6; 11pp; English.
XX
CC The present sequence is an N-terminally truncated polypeptide of human
CC platelet derived growth factor (PDGF)-D, formally known as Vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC Lambda10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of
CC PDGF-D and its proteolytic cleavage for generating an activated truncated
CC form is useful for regulating receptor binding specificity of PDGF-D.
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
XX
XX Sequence 322 AA;
SQ

Query Match 100.0%; Score 737; DB 21; Length 322;
Best Local Similarity 100.0%; Pred No. 1.1e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
Db 191 myldtpyrgsyhdkrskvdlrlndadakyrcptpnysvniireelkianvvpfrcll 250

QY 61 VQRCGNCGGTWNRSCTCNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHE 120
Db 251 vqrcgncgcgtwnrsctcnsqtkvkkylhevlqfepghikrrgraktmalvdiqlhdhe 310

QY 121 RDCICSSRPPR 132
Db 311 rdcicssrppr 322

RESULT 2
AAB48653
ID AAB48653 standard; Protein; 370 AA.
XX
AC AAB48653;
XX
DT 09-MAR-2001 (first entry)
DE Human growth factor homologue zveg4, SEQ ID NO:2.
XX
XX Human; zveg4; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic; chromosome 11q22.3-23.1.
XX
OS Homo sapiens.
XX
XX WO200066736-A1.
PN
XX
XX 09-NOV-2000.
PD
XX
XX 03-MAY-2000; 2000WO-US40047.
PF
XX
XX 03-MAY-1999; 99US-0304216.
PR 10-NOV-1999; 99US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX

PA (ZYMO) ZYMOGENETICS INC.
XX
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
XX WPI: 2000-687541/67.
DR N-PSDB; AAC81555.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Claim 1; Page 110-111; 143pp; English.
PS
XX The invention relates to the human growth factor homologue zveg4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zveg4 or fragments thereof, particularly human zveg4/human zveg3
CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zveg4.
XX
XX Sequence 370 AA;
SQ

Query Match 100.0%; Score 737; DB 21; Length 370;
Best Local Similarity 100.0%; Pred No. 1.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
Db 239 myldtpyrgsyhdkrskvdlrlndadakyrcptpnysvniireelkianvvpfrcll 298

QY 61 VQRCGNCGGTWNRSCTCNSGKTVKKYHEVLQFEPGHIKRRGAKTMAVDIQLDHHE 120
Db 299 vqrcgncgcgtwnrsctcnsqtkvkkylhevlqfepghikrrgraktmalvdiqlhdhe 358

QY 121 RDCICSSRPPR 132
Db 359 rdcicssrppr 370

RESULT 3
AAY96864
ID AAY96864 standard; Protein; 370 AA.
XX
AC AAY96864;
XX
XX 26-SEP-2000 (first entry)
DT
XX
XX SEQ. ID. 37 from WO0034474.
DE
XX
XX Vascular endothelial growth factor; homologue; zveg3; CUB domain;
KW

KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
 KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
 KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
 KW vulnary.
 XX
 OS Homo sapiens.
 XX
 PN WO200034474-A2.
 XX
 PD 15-JUN-2000.
 XX
 PF 07-DEC-1999; 99WO-US28968.
 XX
 PR 07-DEC-1998; 98US-0207120.
 PR 06-JUL-1999; 99US-0142576.
 PR 21-OCT-1999; 99US-0161653.
 PR 12-NOV-1999; 99US-0165255.
 XX
 PA (ZWO) ZWOGENETICS INC.
 XX
 PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 XX
 DR WPI; 2000-423420/36.
 DR N-PSDB; AAA51541.
 XX
 PT Novel zveg3 polypeptides and nucleotides encoding them useful for
 PT stimulating growth of smooth muscle cells and fibroblasts comprising an
 PT epitope bearing portion of a specific amino acid sequence
 XX
 PS Disclosure; Page 164-165; 173pp; English.
 XX.
 CC Polypeptides comprising an epitope-bearing portion human or murine
 CC ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The
 CC growth factors comprise a growth factor domain and a CUB domain (generic
 CC sequence motifs are shown in AAY96859 and AAY96860). The growth factor
 CC domain is characterized by an arrangement of cysteine residues and
 CC beta-strands that is characteristic of the "cysteine knot" structure of
 CC the platelet-derived growth factor (PDGF) family. The CUB domain shows
 CC homology to CUB domains in neuropilins, human bone morphogenetic
 CC protein-1, porcine seminal plasma protein, bovine acidic seminal fluid
 CC protein and Xenopus laevis tolloid-like protein. Structural analysis and
 CC homology predict that ZVEGF3 polypeptides complex with a second
 CC polypeptide to form multimeric proteins. The human zveg3 gene has been
 CC mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth
 CC of fibroblasts or smooth muscle cells, for activating cell surface
 CC PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated
 CC cellular processes. ZVEGF3 is useful for regulating (post-development)
 CC organ growth, regeneration and maintenance, as well as tissue
 CC maintenance and repair processes. ZVEGF3 antagonists are useful for
 CC treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic
 CC limb disease, peripheral vascular disease, myocardial ischemia, vascular
 CC intimal hyperplasia, atherosclerosis, wound healing, chronic liver
 CC disease and haemangioma formation. ZVEGF3 can also be used to modulate
 CC neurite growth and development of the nervous system, and for treating
 CC neurodegenerative diseases.
 XX
 SQ Sequence 370 AA;
 Query Match 100.0%; Score 737; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 1.3e-73;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYLDPYRGSRYSYHDKSKVDLDRINDAKRYSCPTPNYSVNIREEKLANVFFPRCLL 60
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 Db 239 myldcpryrgsrshdkskvldlrrindakryscptprnysvniireelkianvffprcll 298
 |||||||
 QY 61 VQRCGNCGCGTVNWRSCNSGKTVKKYHEVLQEPGHRGRRAKTMALVDIQLDHE 120
 |||||||
 Db 299 vqrcgncgcvtnwrscnsgtkvkkylqfepghkrgraktmalvdiqlldhe 358
 |||||||
 QY 121 RCDICSSRRPR 132

Db 359 rcdicssrrpr 370
 |||||||
 RESULT 4
 AAY71130
 ID AAY71130 standard; Protein; 370 AA.
 XX
 AC AAY71130;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Human Platelet Derived Growth Factor (PDGF)-D protein.
 XX
 KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnary;
 KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
 KW proliferative; activator; proliferation; differentiation; motility;
 KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
 KW atherosclerosis; wound; metastasis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 52..170
 FT /label= CUB_domain
 FT /note= "Participates in protein-protein or carbohydrate
 FT interactions"
 FT Cleavage-site 254..257
 FT /label= Proteolytic_site
 FT /note= "Dibasic motif"
 XX
 PN WO200027879-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-US26462.
 XX
 PR 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Eriksson U, Aase K, Ponten A, Lee X, Untela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX
 DR WPI; 2000-376495/32.
 DR N-PSDB; AAD00738.
 XX
 PT Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX
 PS Claim 25; Fig 8; 111pp; English.
 XX
 CC The present sequence is the complete human platelet derived growth factor
 CC (PDGF)-D, formally known as Vascular Endothelial Growth Factor (VEGF)-G.
 CC It is derived from human foetal lung lamdagt10 cDNA library. It belongs
 CC to the VEGF/PDGF family. It functions as an activator of proliferation,
 CC differentiation, growth and motility of cells, that express PDGF-D
 CC receptor. This sequence is useful for inhibiting the growth of tumours,
 CC that express PDGF-D. Expression of PDGF-D and its proteolytic cleavage
 CC for generating an activated truncated form is useful for regulating
 CC receptor binding specificity of PDGF-D. PDGF-D antagonist is useful for
 CC inhibiting tissue remodelling during the invasion of tumour cells into
 CC normal cells. PDGF-D may be used to treat wounds, atherosclerosis,
 CC metastasis and migration of smooth muscle cells.
 XX
 SQ Sequence 370 AA;

Query Match 100.0%; Score 737; DB 21; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSGYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
|||||
Db 239 myldtprygrsgyhdrkskvdldrlnddakryscptpnysvnireekklanvffprcll 298
|||||

QY 61 VORCGGNCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHE 120
|||||
Db 299 vqrcgncgcgtvnnwrsctcnsghtvkkynhevlqfepghkrrgraktmalvdiqldhhe 358
|||||

QY 121 RDCICSSRPPR 132
|||||
Db 359 rdcicssrppr 370
|||||

RESULT 5
AAB60888
ID AAB60888 standard; protein; 370 AA.
XX
AC AAB60888;
XX
DT 02-APR-2001 (first entry)
XX
DE -Human VEGF-G protein.
XX
KW Vascular endothelial growth factor; VEGF; cancer; cell;
KW angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200100878-A2.
XX
PD 04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US18085.
XX
PR 30-JUN-1999; 99US-0343671.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gearing DP;
XX
DR WPI; 2001-050129/06.
XX
PT New vascular endothelial growth factor family member used for diagnosis
PT and treatment of deregulated cell growth e.g. cancer, disorders
PT involving aberrant angiogenesis e.g. psoriasis, and chronic
PT inflammatory diseases -
XX
PS Claim 2; Fig 1; 142pp; English.
XX
CC The present invention relates to a vascular endothelial growth factor
CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid
CC molecules are used as modulating agents or as targets for
CC developing modulating agents to regulate a variety of cellular
CC processes e.g. cell proliferation, differentiation, migration and
CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,
CC peptidomimetic or nucleic acid are used to treat a subject with
CC aberrant VEGF-G protein or nucleic acid expression or activity
CC e.g. deregulated cell growth, such as cancer, hypertrophic bone
CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,
CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G
CC gene expression is inhibited through the administration of antisense
CC molecules or ribozymes and by targeting the regulatory region of VEGF-G
CC to prevent transcription of the gene in target cells.
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 737; DB 22; Length 370;

Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSGYHDKRSKVDLRLNDADAKRYSCPTPNYSVNIREEKLANVVFPRCLL 60
|||||
Db 239 myldtprygrsgyhdrkskvdldrlnddakryscptpnysvnireekklanvffprcll 298
|||||

QY 61 VORCGGNCGGTNNWRSCTCNSGKTVKKYHEVLQFEPGHKRRGRKTMALVDIQLDHE 120
|||||
Db 299 vqrcgncgcgtvnnwrsctcnsghtvkkynhevlqfepghkrrgraktmalvdiqldhhe 358
|||||

QY 121 RDCICSSRPPR 132
|||||
Db 359 rdcicssrppr 370
|||||

RESULT 6
AAY71128
ID AAY71128 standard; peptide; 200 AA.
XX
AC AAY71128;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #1.
XX
KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis.
XX
OS Homo sapiens.
XX
PN WO200027879-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US26462.
XX
PR 10-NOV-1998; 98US-0107852.
PR 28-DEC-1998; 98US-0113997.
PR 26-AUG-1999; 99US-0150604.
PR 04-OCT-1999; 99US-0157108.
PR 05-OCT-1999; 99US-0157756.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
PI Oestman A, Heldin C;
XX
DR WPI; 2000-376495/32.
DR N-PSDB; AAD00736.
XX
PT Novel polynucleotides encoding a novel growth factor of cells
PT expressing a platelet-derived growth factor, useful for diagnostic and
PT therapeutic applications, e.g. concerning cancer -
XX
PS Claim 25; Fig 4; 111pp; English.
XX
CC The present sequence is an N-terminally truncated polypeptide of human
CC platelet derived growth factor (PDGF)-D, formally known as Vascular
CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
CC lambda2g10 cDNA library. It belongs to the VEGF/PDGF family. It functions
CC as an activator of proliferation, differentiation, growth and motility of
CC cells, that express PDGF-D receptor. This sequence is useful for
CC inhibiting the growth of tumours, that express PDGF-D. Expression of
CC PDGF-D and its proteolytic cleavage for generating an activated truncated
CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
CC

```

XX SQ Sequence 200 AA;
Query Match 96.7%; Score 713; DB 21; Length 200;
Best Local Similarity 97.7%; Pred. NO. 2.9e-71;
Matches 129; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSYHDKSKVDLRDLNDADAKRYSCPTPRNYSVNIRELKLANVFFPRCLL 60
DB 69 MYLDTPRYGRSYHDKSKVDLRDLNDADAKRYSCPTPRNYSVNIRELKLANVFFPRCLL 128

QY 61 VQRCGNGCGGTNNRSCNCGTKVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHE 120
DB 129 VQRCGNGCGGTNNRSCNCGTKVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHE 188

QY 121 RDCDICSSRPPR 132
DB 189 RDCDICSSRPPR 200

RESULT 7
AAB48663
ID AAB48663 standard; Protein; 370 AA.
XX AC AAB48663;
XX DT 09-MAR-2001 (first entry)
XX DE Mouse growth factor homologue zveg4, SEQ ID NO:53.
XX KW Mouse; murine; zveg4; growth factor homologue; VEGF/PDGF family;
XX KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
XX KW neovascularisation; tissue repair; proliferation; differentiation;
XX KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
XX KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
XX KW immunomodulation; hepatic.
XX OS Mus musculus.
XX PN WO2000066736-A1.
XX PD 09-NOV-2000.
XX PF 03-MAY-2000; 2000WO-US40047.
XX PR 03-MAY-1999; 99US-0304216.
XX PR 10-NOV-1999; 99US-0164463.
XX PR 04-FEB-2000; 2000US-0180169.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX WPI; 2000-687541/67.
XX DR N-PSDB; AAC81596.
XX PT Growth factor homologs and the nucleic acids that encode them, useful
XX PT e.g. for treating liver damage, ischemia, multiple sclerosis and
XX PT Alzheimer's disease -
XX PS Example 19; Page 138-140; 143pp; English.
XX CC The invention relates to the human growth factor homologue zveg4
XX CC (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member
XX CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
XX CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)
XX CC characterised by a PDGF cysteine knot structure, and a CUB domain
XX CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
XX CC activity, having mitogenic activity on fibroblasts, vascular smooth
XX CC muscle cells and pericytes, and has also been shown to stimulate bone
XX CC growth. The invention also relates to fusion proteins comprising human
XX CC zveg4 or fragments thereof, particularly human zveg4/human zveg3

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CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents mouse zveg4.
XX SQ Sequence 370 AA;

Query Match 93.1%; Score 686; DB 21; Length 370;
Best Local Similarity 90.2%; Pred. NO. 5.9e-68;
Matches 119; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSYHDKSKVDLRDLNDADAKRYSCPTPRNYSVNIRELKLANVFFPRCLL 60
DB 239 LYLDTPHYGRSYHDKSKVDLRDLNDADAKRYSCPTPRNYSVNIRELKLANVFFPRCLL 298

QY 61 VQRCGNGCGGTNNRSCNCGTKVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHE 120
DB 299 VQRCGNGCGGTNNRSCNCGTKVKKYHEVLQEPGHIKRRGAKTMALVDIQLDHHE 358

QY 121 RDCDICSSRPPR 132
DB 359 RDCDICSSRPPR 370

RESULT 8
AAB60895
ID AAB60895 standard; protein; 370 AA.
XX AC AAB60895;
XX DT 02-APR-2001 (first entry)
XX DE Human VEGF-G protein.
XX KW Vascular endothelial growth factor; VEGF; cancer; cell;
XX KW angiogenesis.
XX OS Homo sapiens.
XX PN WO200100878-A2.
XX PD 04-JAN-2001.
XX PF 29-JUN-2000; 2000WO-US18085.
XX PR 30-JUN-1999; 99US-0343671.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Gearing DP;
XX WPI; 2001-050129/06.
XX PT New vascular endothelial growth factor family member used for diagnosis
XX PT and treatment of deregulated cell growth e.g. cancer, disorders
XX PT involving aberrant angiogenesis e.g. psoriasis, and chronic
XX PT inflammatory diseases -

```

```

CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents mouse zveg4.
XX SQ Sequence 370 AA;

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PS Claim 2; Fig 8; 142pp; English.

XX The present invention relates to a vascular endothelial growth factor

CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid

CC molecules are used as modulating agents or as targets for

CC developing modulating agents to regulate a variety of cellular

CC processes e.g. cell proliferation, differentiation, migration and

CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,

CC peptidomimetic or nucleic acid are used to treat a subject with

CC aberrant VEGF-G protein or nucleic acid expression or activity

CC e.g. deregulated cell growth, such as cancer, hypertrophic bone

CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,

CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G

CC gene expression is inhibited through the administration of antisense

CC molecules or ribozymes and by targeting the regulatory region of VEGF-G

CC to prevent transcription of the gene in target cells.

XX

SQ Sequence 370 AA;

Query Match 92.4%; Score 681; DB 22; Length 370;

Best Local Similarity 89.4%; Pred. No. 2.1e-67;

Matches 118; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MYLDPYRGSRVHDKRSKVDLRLNDADAKRYSCTPRNVSVNIREELKLANVVFPRCLL 60

Db :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

239 lyldtphyrgrsyhdkrskvdlrldndvkrystcprnhsvnlreekltnavffprcll 298

QY 61 VORCGNCGGTVNRSCNCGTKVKKYHEVLQFEPGHKRGRAKTMALVDIQLDHHE 120

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

299 vqrcgncgcgtvwnksctessgktvkkylhevlqfepghkrrgkaknmpldvldiqdhhe 358

QY 121 RDCICSSRRPPR 132

Db ||||||| |||||||

359 rdcicssrrppr 370

RESULT 9

AAAY71132

ID AAY71132 standard; peptide; 66 AA.

AC AAY71132;

XX

DT 08-SEP-2000 (first entry)

XX

DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #3.

XX

KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;

KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;

KW proliferative; activator; proliferation; differentiation; motility;

KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;

KW atherosclerosis; wound; metastasis.

XX

OS Homo sapiens.

XX

PN WO200027879-A1.

XX

PD 18-MAY-2000.

XX

PF 10-NOV-1999; 99WO-US26462.

XX

PR 10-NOV-1998; 98US-0107852.

PR 28-DEC-1998; 98US-0113997.

PR 26-AUG-1999; 99US-0150604.

PR 04-OCT-1999; 99US-0157108.

PR 05-OCT-1999; 99US-0157756.

XX

PA (LUDWIG-) LUDWIG INST CANCER RES.

XX

PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.

XX

PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;

PI Oestman A, Heldin C;

XX

DR WPI; 2000-376495/32.

XX N-PSDB; AAD00739.

XX

PT Novel polynucleotides encoding a novel growth factor of cells

PT expressing a platelet-derived growth factor, useful for diagnostic and

PT therapeutic applications, e.g. concerning cancer -

PS Disclosure; Fig 2; 111pp; English.

XX

XX The present sequence is the partial C-terminal end polypeptide #3, of

CC human platelet derived growth factor (PDGF)-D, formally known as

CC Vascular Endothelial Growth Factor (VEGF)-G. It is derived from a human

CC expressed sequence tag (EST) A1488780. It belongs to the VEGF/PDGF

CC family. It functions as an activator of proliferation, differentiation,

CC growth and motility of cells, that express PDGF-D receptor. This sequence

CC is useful for inhibiting the growth of tumours, that express PDGF-D.

CC Expression of PDGF-D and its proteolytic cleavage for generating an

CC activated truncated form is useful for regulating receptor binding

CC specificity of PDGF-D. PDGF-D antagonist is useful for inhibiting tissue

CC remodelling during the invasion of tumour cells into normal cells.

CC PDGF-D may be used to treat wounds, atherosclerosis, metastasis and

CC migration of smooth muscle cells.

XX

SQ Sequence 66 AA;

Query Match 51.6%; Score 380; DB 21; Length 66;

Best Local Similarity 100.0%; Pred. No. 6.4e-35;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 NCCGCVNWRSCNCGTKVKKYHEVLQFEPGHKRGRAKTMALVDIQLDHHERCDIC 126

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1 nccgcvnwrscnsgktvkkylhevlqfepghkrrgkraktmalvdidhhercdic 60

QY 127 SSRPPR 132

Db |||||||

61 ssrppr 66

RESULT 10

AAAB10639

ID AAB10639 standard; Protein; 374 AA.

XX

AC AAB10639;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X protein for expression in mammalian systems.

XX

KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN WO200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

PA (JANC) JANSSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

QY 119 HERCDCIC 126
 Db 326 heeecdvc 333

RESULT 14
 AAY33679
 ID AAY33679 standard; Protein; 345 AA.
 XX
 AC AAY33679;
 XX
 DT 11-JAN-2000 (first entry)
 XX
 DE Human VEGF-E protein.
 XX
 KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO9947677-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US05190.
 XX
 PR 17-MAR-1998; 98US-0040220.
 PR 02-NOV-1998; 98US-0184216.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ferrara N, Kuo SS;
 XX
 DR WPI; 1999-580306/49.
 DR N-PSDB; AAZ23691.
 XX
 PT New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy -
 XX
 PS Claim 1; Fig 2; 122pp; English.
 XX
 CC This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.

SQ Sequence 345 AA;
 Query Match 44.68; Score 328.5; DB 20; Length 345;
 Best Local Similarity 49.2%; Pred. No. 2.3e-28;
 Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
 QY 1 MYLDTPRYGRSY-IDRKSK-VDLRLNDDAKRYSCPTPNYSVNIREELKLANVVFPRC 58
 Db 215. lyrtwqlgkafvgrksrvvdlnllceevrlyscptpnfsvsireelkrttdtlfwpgc 274
 QY 59 LLVORCGNCGCGTWNRSCTNSGKTVKYHEVLQFEPGHKKRGRAKTMALVDIQLDH 118
 Db 275 llvkrcgncaccihncnecqcvpskvtkyhevlqlrp---ktgvrghksltdvaleh 331
 QY 119 HERCDCIC 126
 Db 332 heeecdvc 339

RESULT 15
 AAY41766
 ID AAY41766 standard; Protein; 345 AA.
 XX
 AC AAY41766;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO200 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.

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 About: Results were produced by the GenCore software, version 4.5,
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Search information block:

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Query length: 132

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Database sequences: 10228115

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gb_est53:AW968905	+	460.00	940.41	2.9e-43	360	AW968905 EST380981 MAGE resequ
gb_est8:AA488780	+	380.00	778.74	2.9e-34	360	AA488780 aa54c10.r1 NCI_CGAP_G
gb_est8:BF021679	+	324.50	659.84	1.2e-27	523	BF021679 uy50f05.y1 NCI_CGAP_L
gb_est102:BG609411	+	322.50	658.08	2.3e-27	556	BG609411 33251 MARC IPTG Sus s
gb_est84:BF151355	+	309.50	627.96	7.4e-26	564	BF151355 uz15b12.y1 NCI_CGAP_M
gb_est28:AL047637	+	301.50	617.48	2.8e-25	304	AL047637 DKF2p586j0421.r1 586
gb_est81:BE958470	+	294.50	597.57	3.6e-24	523	BE958470 601644787F1 NIH_MGC_5
gb_gss4:CN80458A	-	291.00	583.53	2.2e-23	1036	AL304867 Tetradonon nigroviridis
gb_est98:BG243001	+	275.50	552.65	1.2e-21	910	BG243001 602355974F1 NCI_CGAP_M
gb_est83:BF102859	+	272.50	551.24	1.4e-21	851	BF102859 601646827F1 NIH_MGC_6
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gb_est80:BE914552	+	184.00	364.02	3.7e-11	799	BE914552 60165653F1 NCI_CGAP_M
gb_est84:BF163629	+	179.00	352.44	1.6e-10	902	BF163629 601769732F1 NCI_CGAP_M
gb_est17:BG118707	+	178.50	350.70	2.0e-10	968	BG118707 602348280F1 NIH_MGC_9
gb_est73:BE374398	+	163.00	329.38	3.2e-09	324	AL1020581 us96c08.r1 Soares.M
gb_est44:AW210331	+	124.00	266.55	1.0e-05	521	BE374398 601227568F1 NCI_CGAP_M
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gb_est15:AA759138	-	108.50	213.57	0.0089	425	AA759138 ah78f03.s1 Soares.Les
gb_est83:BF117246	+	105.50	219.39	0.0042	126	BF117246 uz07a06.y1 NCI_CGAP_M
gb_gss31:AE686072	+	95.00	178.59	0.7902	858	AZ686072 ENTK57TF Entamoeba h
gb_est99:BG353561	+	92.00	178.56	0.7929	459	BG353561 947043E01.y2 947 - 2
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gb_est30:AA085049	+	91.00	175.56	1.17	504	AA085049 AU085049 Cryptomeria
gb_est7:AA425486	+	91.00	175.46	1.18	509	AA425486 zw46b06.r1 Soares.tota
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gb_est87:BF423344	+	90.00	174.11	1.40	473	BF423344 sr37b04.y1 Gm-cl051 G
gb_est83:BF073247	+	90.00	172.91	1.64	534	BF073247 219851 MARC 2B0V Bos
gb_est22:AI1583995	+	90.00	169.35	2.58	765	AI1583995 ts08c03.x1 NCI_CGAP_P
gb_est22:BF262012	+	90.00	168.62	2.84	823	BF262012 HV_CEA002N05f Hordeum
gb_est74:BE424082	-	89.50	173.16	1.59	469	BE424082 WHE0068.G05 M102S Whea
gb_est53:AW914212	+	89.00	173.26	1.56	418	AW914212 EST345516 Normalized
gb_est4:AA240232	+	89.00	173.00	1.62	429	AA240232 my24b02.r1 Barstead mc
gb_est7:AA420061	+	89.00	171.91	1.86	479	AA420061 vf50b05.r1 Soares.mamm
gb_est89:BF523368	+	89.00	171.48	1.96	500	BF523368 UI-R-G0-uh-c-05-0-UI.R

gb_est80:BE864788	+	89.00	170.56	2.21	549	BE864788 UI-M-BH1-alu-c-12-0
gb_est48:AW555889	-	89.00	170.19	2.32	570	AW555889 L0260G12-3 Mouse Ne
gb_est87:BF448004	-	89.00	170.19	2.32	570	BF448004 nae3a0a08.x1 Lupski
gb_est96:BG087899	+	89.00	169.84	2.42	590	BG087899 H3146C02-5 NIA Mous

seq_name: gb_hlc:AK003359

seq_documentation_block:

LOCUS AK003359 1796 bp mRNA HTC 08-FEB-2001
 DEFINITION Mus musculus 18 days embryo cDNA, RIKEN full-length enriched
 library, clone:1110003109, full insert sequence.

ACCESSION AK003359

VERSION AK003359.1 GI:12833975

KEYWORDS CAP trapper.

SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,

clone.lib:RIKEN full-length enriched mouse cDNA library

clone:1110003109.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (sites)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning

Methods Enzymol. 303, 19-44 (1999)

REFERENCE

2 (sites)

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

REFERENCE

3 (sites)

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T.,

Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,

Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

REFERENCE

4 (sites)

The RIKEN Genome Exploration Research Group Phase II Team and

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 (bases 1 to 1796)

REFERENCE

AUTHORS

Arakawa,T., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,

Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F.,

Imotani,K., Ishii,Y., Itoh,M., Kato,H., Kawai,J., Kawai,J.,

Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,

Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y.,

Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H.,

Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,

Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

further details.

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

COMMENT

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGACAGAGAGCCGACACGATCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to R0t = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5', GAGACAGAGAGAGATCCAGAGCTCAATTAATTAATTAACCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

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      LDTPHYRGSYHDKRSKVDLRLNDDVKRYSCTPRNHSHVNLREELKLNVAFFPCLL
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BASE COUNT 546 a 378 c 403 g 469 t
ORIGIN
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:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
899 TTGATCTGGACACCCCTCATATTAGAGGAGGATACACCATGATCGAA 948
17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
949 GTCAAAAGTGGACCTGGACAGGCTCAATGATGATGTCGAAGCGTTACAGTT 998
34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
999 GCACCTCCAGGAATCACTCTGTGAACCTCAGGGAGAGGCTGAAGCTGACC 1048
51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1049 AATCAGCTCTCTCCACAGATGCTCTCTGTCGACGCGCTGTGGTGCAA 1098
67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1099 CTGTGGTTCGGAAGTGTCAACTGGAAGTCTCGCACATGCAGCTCAGGGA 1148
84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1149 AGACAGTGAAGAAGTATCATGAGGTATTGAAGTTTGAGCCTGGACATTC 1198
101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1199 AAGAGAGGGGCAAGCTGAAGAATATGGCTCTTGTGATATCCAGCTGGA 1248
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117 pHHisGluArgCysAspCysLeuValGlnArgCysSerArgProProArg 132
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1249 TCATCATGAGCGATGTGACTGTATCTCAGCTCAAGACCACTCGA 1294
seq_name: gb_est53:AW968905
seq_documentation_block:
LOCUS AW968905 560 bp mRNA EST 01-JUN-2000
DEFINITION EST380981 MAGE resequences, MAGJ Homo sapiens cDNA, mRNA sequence.
ACCESSION AW968905
VERSION AW968905.1 GI:8158746
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 560)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 258
Seq primer: Forward.
FEATURES
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    /clone_lib="MAGE resequences, MAGJ"
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alignment_scores:
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  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-662-783-4 x AW968905 ..
Align seg 1/1 to: AW968905 from: 1 to: 560
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2 GTCCTCTTCCACGCTGCCCTCCTCGTCAGCGCTGTGGAGAAATTTGG 51
69 yCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrV 86
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
52 CTGTGGAACGTCAACTGGAGGTCTGCACATGCAATTCAGGAAACCG 101
86 alLysLysTyrHisGluValLeuGlnPheGluProGlyHisIleLysArg 102
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
102 TGAAGAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCCATCAAGAG 151
103 ArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAspHisH 119
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
152 AGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGATCACA 201
119 sGluArgCysAspCysLecCysSerSerArgProProArg 132
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202 TGAACGATGTGATTGTATCTGCAGCTCAAGACCACTCGA 241
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mRNA sequence.
ACCESSION AA488780
VERSION AA488780.1 GI:2218382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 360)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 358.
FEATURES
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/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGCGCGCTCATTTTTTTTTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
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ORIGIN
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US-09-662-783-4 x AA488780
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67 AsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerG1 83
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1 AATGTGGTGTGGAACTGTCAACTGGAGGTCTGCACATGCAATTCAGG 50
|||||
83 YLysThrValLYsLYsThrHisGluValLeuGlnPheGluProGlyHisI 100
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100 leLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeu 116
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```

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101 TCAAGAGGAGGGGTAGAGCTAAGACCATGCTCTAGTTCACATCCAGTTG 150
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117 AspHisHisGluArgCyspCyspCysIleCysSerSerArgProProArg 132
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151 GATCACCATGTAAGCATGTATTGTATCTGCAGCTCAAGACCATCGA 198
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seq_name: gb_est82:BF021679
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LOCUS BF021679 523 bp mRNA EST 29-DEC-2000
DEFINITION uy50f05.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3663009 5',
similar to FR:Q9QY71 Q9QY71 FALLOTEIN. ;, mRNA sequence.
ACCESSION BF021679
VERSION BF021679.1 GI:10753011
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 523)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
MG1:1423777
Seq primer: -40RP from Gibco
High quality sequence stop: 452.
FEATURES
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1..523
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Site.2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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ORIGIN
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131 CTCTACAGCCACATGGCAGCTTTTGGCAGGCTTCTCTGTATGGAA 180
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16 GlySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
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181 AAAAAAGCAAGTGGTGAATCTGAATCTCTCTCTCTCTCTCTCTCTCTCT 230
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32 yrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
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49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
 :
 281 AGGACAGATACCATATTCTGCCAGGTGTCTCTCTGGTCAAGCGCTGTGG 330

65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
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 331 AGGAAATGTGCTGCTGTCCTCCATAATTCGAATGATGTCTCAGTGTGCC 380

82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
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 381 CACGTAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCA... 427

99 HistLeysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleG1 115
 :
 428AAAACGTGGAGTCAAGGATTCGATAAGTCACTCACTGATGTGGC 471

115 nLeuAspHisGluArgCysAspCysIleCys 126
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472 TCTGGAACACACGAGGAATGACTGTGTGT 505

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 VERSION BG609411.1 GI:13659390
 KEYWORDS EST.
 SOURCE Pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 556)
 AUTHORS Fahrnkruug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
 and Keele, J.W.
 TITLE Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt.trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAACACAGCTATGACCAT
 BACKWARD: GTTTCACGACGACGACG
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 Seq primer: ATTTAGTGACACTATAG.
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 Library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."

FEATURES
 source

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 ORIGIN

alignment_scores:

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 Ratio: 3.291 Gaps: 3
 Percent Similarity: 76.562 Percent Identity: 48.438

alignment_block:

US-09-662-783-4 x BG609411 ..

Align seg 1/1 to: BG609411 from: 1 to: 556

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 :
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16 gLysSerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArgT 32
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 232 AAATCCAGAGTGTGGATCTGAACCTTCTCAAGAGAAGAGTGGCTAT 281

32 yrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
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 282 ACAGCTGCACCCCTAGGAACCTTTTCAGTGTCTATCAGGGAAGAGCTGAAG 331

49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
 :
 332 AGAACAGACACCATCTTCTGCCAGGCTGCTCTCTCTCAAGCGTGTGG 381

65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
 |||||
 382 CGGAACAGTGTGCTGCTGCATGCACACCTGCATGAGTGTGAGTGTGCC 431

82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
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 432 CCAGCAAGTCAACCAAGAAATATCAGGAGTCTCTCAGTTGAGACCC... 478

99 HistLeysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleG1 115
 :
 479AAGACAGTGTCCGGGGGCTGCACAAGTCCCTCACCGAGTGGC 522

115 nLeuAspHisGluArgCysAspCysIleCys 126
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523 CCTGGAGCACCCAGGAGGTGTGACTGGGTGTGC 556

seq_name: gb_est84:BF151355

seq_documentation_block:

LOCUS BF151355 564 bp mRNA EST 29-DEC-2000
 DEFINITION uz15b12.y1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669119 5',
 similar to TR:Q9QY71 Q9QY71 FALLOTEIN.; mRNA sequence.

ACCESSION BF151355
 VERSION BF151355.1 GI:11032750
 KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 564)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapb-remail.nih.gov

Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1429887

Seq primer: -40RP from Gibco

High quality sequence stop: 436.

Location/Qualifiers

FEATURES

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: Noti; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT      157 a 130 c 140 g 137 t
ORIGIN

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US-09-662-783-4 x BF151355 ..
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178 CTCTACAGCCACACATGGCAGCTTTTGGCAAGGCTTCTCTGTATGGAA 227

16 GlySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
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228 AAAAGCAAGGTGGTAATCTGAATCTCTCAAGGAAGGTAATAACTCT 277

32 YrSerCysThrProArgAsnTyrSerValAsnIleAargGluLeuLys 48
   :|||  |||  ::  |||:::  ::  ::
278 ACAGTGCACACCCCGGAATCTCAGTGTCCATACGGGAAGAGCTAAG 327

49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnAargCysG 65
   ::::  ::  |||  ::  |||:::  ::  ::
328 AGGACAGATACCATATCTGGCAGGTTCTCTCGTCAAGCGCTGTGG 377

65 YGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
   :|||  |||  ::  |||:::  ::  ::
378 AGAAATGTGCTGTGTCTCATTAATTCGAATGCAATGCTCAGTGTGTC 427

82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
   :|||  |||  ::  |||:::  ::  ::
428 CAGGTAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCA... 474

99 HisIleLysAargGlyArgAlaLysThrMetAlaLeuValAspIleG 115
   :|||  |||  ::  |||:::  ::  ::
475 .....AAAAGCTGGATCAAGGATTCGATAAAGTACTCAATGATGTGC 518

115 nLeuAspHisHisGluAargCysAspCysIleCys 126
   :|||  |||  ::  |||:::  ::  ::
519 TCTTGAACACCCAGGAGGATGTGACTGGGTGTGT 552

seq_name: gb_est28:AL047637

seq_documentation_block:
LOCUS      AL047637      304 bp      mRNA      EST      01-MAR-2000
DEFINITION DKF2p586J0421_r1 586 (synonym: hutel) Homo sapiens cDNA clone
ACCESSION  AL047637
VERSION    AL047637.1 GI:4728633
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS      Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE        EST (Ottenwaelder, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Ottenwaelder B
              MIPS
              Am Klopferspitz 18a D-82152 Martinsried, Germany
              This is the 5' sequence of the clone insert
              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
              Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
              sequenced by MediGenomix (Martinsried/Germany) within the cDNA
              sequencing consortium of the German Genome Project. No s1 sequence
              available.
              This clone (DKFZp586J0421) is available at the RZPD in Berlin.
              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
              Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
  source
  1..304
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="DKFZp586J0421"
    /clone_lib="586 (synonym: hutel)"
    /tissue_type="uterus"
    /dev_stage="adult"
    /lab_host="DH10B"
    /note="Vector: pSport1; Site_1: Noti; Site_2: Sali/MLUI"

BASE COUNT      86 a 68 c 80 g 70 t
ORIGIN

alignment_scores:
  Quality: 301.50      Length: 100
  Ratio: 3.769        Gaps: 1
Percent Similarity: 80.000 Percent Identity: 53.000

alignment_block:
US-09-662-783-4 x AL047637 ..
Align seg 1/1 to: AL047637 from: 1 to: 304

27 AspAspAlaLysArgTyrSerCysThrProArgAsnTyrSerValAsnrl 43
   ::::  ::  |||  ::  |||:::  ::  ::
2   GAGGAGGTAAGATTATACAGTCGCACACCTCGTAACCTCTCAGTGCCAT 51

43 eaargGluGluLeuLysLeuAlaAsnValValPhePheProAargCysLeuL 60
   :|||  |||  ::  |||:::  ::  ::
52 AAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCC 101

60 euValGlnAargCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpAarg 76
   :|||  |||  ::  |||:::  ::  ::
102 TGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCACAATTCGAAT 151

77 SerCysThrCysAsnSergLysThrValLysLysLysLysLysHisGluVal 93
   :|||  |||  ::  |||:::  ::  ::
152 GAATGTCATGTGTCCCAAGCAAGTACTAAAAAATACACAGAGTCCT 201

93 uGlnPheGluProGlyHisIleLysAargGlyArgAlaLysThrMeta 110
   :|||  |||  ::  |||:::  ::  ::
202 TCAGTTGAGACCA.....AAGACCGGTGTGACGGGATTCACAAAT 242

110 laLeuValAspIleGlnLeuAspHisHisGluAargCysAspCysIleCys 126
   :|||  |||  ::  |||:::  ::  ::
243 CACTACCCAGCGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTC 292

seq_name: gb_est81:BE958470
seq_documentation_block:
LOCUS      BE958470      523 bp      mRNA      EST      04-OCT-2000
DEFINITION 601644787P1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930045 5',
ACCESSION  BE958470
VERSION    BE958470
KEYWORDS  mRNA sequence.
SOURCE    BE958470.1 GI:10569175

```

Align seg 1/1 to reverse of: CNS04S8A from: 1 to: 1036

```

20 ValaspLeuAspArgLeuAsnAspAlaLysArgTyrSerCysThrPr 36
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
406 GTTGATCTCAACCGTCTCATGATGATGTCAAGCGCTACAGCTGCACGCC 357

36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnValV 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
356 CCGTAACACTACTCTGAATCTCAAAAGAGCTAAGGCCACAACAGCTA 307

53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
306 TTTTCTCCACGCTGTTGCTTTGACACGATGTTGGTGGCAACTGTGA 257

70 CysGlyThrValAsnTyrArgSer...CysThrCysAsnSerGlyLysThr 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
256 TGTGGACCAACAGCACTGGAATAACACTGCGCTGTCAAGGCCCAATCA 207

86 ValLysLysTyrHisGluVal 92
::: ||| |||||
206 GCACCAAACTACATGAAGTA 186

seq_name: gb_est98:BG243001

seq_documentation_block: 910 bp mRNA EST 13-FEB-2001
LOCUS BG243001
DEFINITION 6023597F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
mRNA sequence.
ACCESSION BG243001
VERSION BG243001.1 GI:12752725
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10323 row: d column: 19
High quality sequence stop: 690.
FEATURES
source
Location/Qualifiers
1..910
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4483938"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: Sali;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 242 a 220 c 250 g 198 t
ORIGIN

alignment_scores:
Quality: 275.50 Length: 119
Ratio: 2.900 Gaps: 3
Percent Similarity: 79.832 Percent Identity: 51.261

alignment_block:
US-09-662-783-4 x BG243001

```

Align seg 1/1 to: BG243001 from: 1 to: 910

```

10 GlyArgSerTyr...HisAspArgLysSerLys...ValaspLeuAspAr 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
149 GCGAAGGCTTTCTGTATGGGAAAAAAGCAAGTGGTGAATCTGAATCT 198

24 gluAsnAspAspAlaLysArgTyrSerCysThrProArgAsnTyrSerV 41
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
199 CCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCTCAG 248

41 alAsnIleArgGluGluLeuLysLeuAlaAsnValValPhePheProArg 57
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
249 TGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGT 298

58 CysLeuLeuValGlnArgCysGlyGlyAsnCysGlyCysGlyThrValAs 74
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
299 TGTCTCCCTGGTCAAGCGCTGTGGAGAAA..TGTGCTGTGTCTCCATAA 347

74 nTrrArgSerCysThrCysAsnSerGlyLysThrValLysLysTyrHisG 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
348 TTGCAATGAATGTCAGTGTGCCACGTAAGTTACAAAAAAGTACCATG 397

91 luValLeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
398 AGGTCTCTTCAGTTGAGACCA.....AAAACCTGAGTCAAGGGA.TTG 437

108 ThrMetAlaLeuValAspIleGlnLeuAspHisGluArgCysAspCy 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
438 CATAAGTCACTCACTGATGTGGCTCTGGNACACACGAGGAATGTGAC 487

124 sileCys 126
488 TGTGTGT 494

```

seq_name: gb_est83:BF102859

```

seq_documentation_block:
LOCUS BF102859 851 bp mRNA EST 19-OCT-2000
DEFINITION 601646827F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073095 5',
mRNA sequence.
ACCESSION BF102859
VERSION BF102859.1 GI:10885385
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM921 row: f column: 08
High quality sequence stop: 529.
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Location/Qualifiers
1..851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4073095"
/clone_lib="NIH_MGC_60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site:1: SfII (ggccgctggcc); Site:2: SfII (ggccattatggcc

```



```

KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE 1 (bases 1 to 447)
NATIONAL CANCER INSTITUTE, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1064727
Seq primer: -40RP from Gibco
High quality sequence stop: 402.
FEATURES
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1..447
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3169267"
/clone_lib="Soares_NMEBA_branchial_arch"
/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/note="vector: pT7T3d-Pac (Pharmacia) with a modified
polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAACTCTGAAGTGGGCGCGCATGTCATTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
constructed and normalized by Bento Soares and M.Patima
Bonaldo."
BASE COUNT 126 a 104 c 108 g 109 t
ORIGIN
..
alignment_scores:
Quality: 264.00 Length: 99
Ratio: 3.342 Gaps: 2
Percent Similarity: 79.798 Percent Identity: 51.515
alignment_block:
US-09-662-783-4 x BF011835
..
Align seg 1/1 to: BF011835 from: 1 to: 447
1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyr...HisAspAr 16
:::||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
115 CTCACAGCCACACATGCGAGCTTTTGGCAAGGCTTCTCTGTATGGGA 164
16 glySerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArgT 32
:::||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
165 AAAACGAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGTAAACTCT 214
32 yfSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
215 ACAGCTGCACACCCGCACTTCTCAGTGTCCATACGGGAAGCTAAAG 264
49 LeuAlaAsnValPhePheProArgCysLeuLeuValcIcloArgCysG1 65
:::||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
265 AGGACAGATACCATATCTGGCCAGGTTGTCTCTGTCAAGCGCTGTGG 314
65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|

```

```

315 AGGAAATTGTGCTGTGTCTCCATAAATGCAATGAATGTCAGTGTGTCC 364
82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluPro 97
||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
365 CACGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGAGACCA 411
seq_name: gb_gss3:CNS024MX
seq_documentation_block:
LOCUS CNS024MX 877 bp DNA GSS 12-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
235A22 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL180978
VERSION AL180978.1 GI:7819035
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 877)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 877)
AUTHORS Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 877)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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1..877
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="235A22"
/clone_lib="G"
/note="Genoscope sequence ID : COAG235BAL1SP1-end :
PUC-Ori"
BASE COUNT 229 a 207 c 188 g 248 t 5 others
ORIGIN
..
alignment_scores:
Quality: 231.00 Length: 211
Ratio: 2.625 Gaps: 5
Percent Similarity: 41.706 Percent Identity: 26.540
alignment_block:
US-09-662-783-4 x CNS024MX/rev
..
Align seg 1/1 to reverse of: CNS024MX from: 1 to: 877
25 LeuAsnAspAlaLysArgTyrSerCysThrProArgAsnTyrSerVa 41
||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
651 CTGAGGATGAAGTGGACTGTACACTGCACACCGCGCAACTTCTGT 602
41 lAsnIleArgGluGluLeuLysLeuAlaAsnValPhePheProArgC 58
||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
601 GTCTTTGCTGAGGAGCTGAAGAGGACCGATGTAATTTTCTGCCAAGCT 552

```

```

58 ysLeuLeuValGlnArgCysGlyAsnCysGlyCysGlyThrValAsn 74
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
551 GCCTCCTGGTGAATCGTGTCGGCGAAACTGCGCTGCTCTCACGCC 502
75 TrpArgSerCysThrCysAsnSerGlyLysThrValLysLysTyrHisG1 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
501 TGCATGACTGCCAGTCCGTTCCACCAGGCTCACGAAGAATATCATGA 452
91 uVal.....LeuGlnPheGluProGlyH 99
|||||:|||||:|||||:|||||:|||||:|||||:
451 GGTAAATGCTAGCACTTCATCTGAGGATGATGTTTCGTTTGGCTGCC 402
99 isleLys.....ArgArgGly..... 104
|||||:|||||:|||||:|||||:|||||:|||||:
401 TTTTAAAGATTTTGAATGCGCGTTTGGAACTTCACAAATTTCTCTGTT 352
104 ..... 104
351 GCCATTACACAATACTACAATKCCAGACACTGTGAAATGTACAAATACTT 302
105 .....ArgAlaLysThr..... 108
|||||:|||||:|||||:|||||:|||||:|||||:
301 ATCTGACTTGAATAATTCAGATCTGAGACGCAAAATCCACTTACACTGCA 252
108 ..... 108
251 TATTTGTTTAAACAACAAATCAACAATCAAGACCAAGCTAAATG 202
108 ..... 108
201 GCATTTGATCGATAATATGATCAGCTTTAAGATGAAATGTTTGATGCCA 152
108 ..... 108
151 ACATGTTGTGCAGGTTCTGCTGTAACATCGAATGGTGGCAAGGCC 102
109 .....MetAlaLeuValAspIleGlnLeuAspHisGluArgCysAsp 123
|||||:|||||:|||||:|||||:|||||:|||||:
101 TGCAAGAATCGTTGACCGAGCTGCCCTTAGAACACACCAAGAAATGCGCC 52
124 CystLeCysSerSerArg.....ProPro 131
|||||:|||||:|||||:|||||:|||||:|||||:
51 TGCCTGTGTAAGATGACTGGGACTGACCTCCG 19

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seq_name: gb_gss23:AZ237000

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seq_documentation_block: 413 bp DNA GSS 14-JUN-2000
LOCUS AZ237000
DEFINITION RPI-23-7102.TV RPI-23 Mus musculus genomic clone RPI-23-7102,
DNA sequence.
ACCESSION AZ237000
VERSION AZ237000
KEYWORDS AZ237000.1 GI:8545046
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 413)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPI-23
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPI-23. For BAC
library availability, please contact Pieter de Jong

```

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Reseach Genetics (http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html). BAC end page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html

Plate: 71 row: 0 column: 2
Seq primer: T7
Class: BAC ends.

FEATURES

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Location/Qualifiers
1..413
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-23-7102"
/clone_lib="RPI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 112 a 88 c 78 g 135 t
ORIGIN

alignment_scores:

Quality: 201.00 Length: 86
Ratio: 3.295 Gaps: 4
Percent Similarity: 70.930 Percent Identity: 53.488

alignment_block:

US-09-662-783-4 x AZ237000/rev ..

Align seg 1/1 to reverse of: AZ237000 from: 1 to: 413

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55 PheProArg.....CysLeuLeuValGlnArgCysGlyGlyAsnCysG1 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
379 TTTCCAAGGGTTTACTCACTCATCAACCAAGG..... 347
69 yCysGlyThrValAsnTrpArgSerCysThrCysAsn.SerGlyLysThr 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 ...GGAATGGGTGAGTGGCATTTGGCTGACTTAATCAAGGGCTTCT 301
86 ValLysLysTyrHisGlu.....ValLeuGlnPheGluPr 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
300 AACAGGAATATATCTTCTATCCTTTATTGTAGGTATTGAAGTTTGAGCC 251
97 oGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeuValAspI 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
250 TGGACATTTCAAGAGAGAGGCAAGCTAAGAATATGCTCTTGTGATA 201
114 leGlnLeuAspHisHisGluArgCysAspCysIleCysSerSerArgPro 130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
200 TCCAGCTGGATCAAAAAGAAAGATGTGACTGTATCTGCAGCTCAAGACCA 151
131 ProArg 132
|||||
150 CCTCGA 145

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 11.6 Seconds
(without alignments)
389.804 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLDPYRGSRHYDRKSKV.....DTQLDHERCDCICSSRPPR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	13.6	148	1	VEGH_ORFN7
2	95.5	13.0	188	1	VEGB_MOUSE
3	94	12.8	213	1	PDGA_RABIT
4	93	12.6	419	1	VEGC_HUMAN
5	92	12.5	415	1	VEGC_MOUSE
6	89	12.1	204	1	PDGA_RAT
7	89	12.1	211	1	PDGA_HUMAN
8	89	12.1	211	1	PDGA_MOUSE
9	85.5	11.6	188	1	VEGB_HUMAN
10	84.5	11.5	133	1	VEGH_ORFN2
11	83	11.3	226	1	PDGA_XENLA
12	81	11.0	241	1	PDGB_SHEEP
13	80	10.9	164	1	VEGE_CAVPO
14	79	10.7	241	1	PDGB_MOUSE
15	78	10.6	225	1	PDGB_RAT
16	77	10.4	77	1	MT2_VICFA
17	77	10.4	79	1	MT2_CICAR
18	77	10.4	146	1	VEGE_SHEEP
19	77	10.4	190	1	VEGE_BOVIN
20	77	10.4	245	1	PDGB_FELCA
21	76.5	10.4	1790	1	LMBI_DROME
22	76	10.3	241	1	PDGB_HUMAN
23	74	10.0	77	1	MT1A_VICFA
24	74	10.0	82	1	MT2B_LYCES
25	74	10.0	215	1	VEGE_HUMAN
26	73.5	10.0	82	1	MT2_ORYSA
27	73.5	10.0	158	1	PLGF_MOUSE
28	73	9.9	78	1	MT2_ACTCH
29	73	9.9	79	1	MT2_MALDO
30	73	9.9	170	1	PLGF_HUMAN
31	72	9.8	80	1	MT2_RICCO
32	71	9.6	77	1	MTA_TRIRP
33	71	9.6	78	1	MT2_MUSAC

34	71	9.6	190	1	VEGF_PIG
35	71	9.6	190	1	VEGF_RAT
36	71	9.6	677	1	SP87_DICDI
37	70.5	9.6	75	1	MT1_PEA
38	70.5	9.6	214	1	VEGF_MOUSE
39	70	9.5	80	1	MT2_BRARP
40	70	9.5	80	1	MT2_BRARP
41	70	9.5	81	1	MT2A_ARATH
42	70	9.5	226	1	TSIS_SMSAV
43	69.5	9.4	1069	1	ENTK_MOUSE
44	69	9.4	80	1	MT1_CORAR
45	69	9.4	84	1	MT22_ORYSA

ALIGNMENTS

RESULT 1	VEGH_ORFN7	STANDARD;	PRT;	148 AA.
ID	VEGH_ORFN7			
AC	P52585;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.			
GN	A2R.			
OS	Orf virus (strain NZ7) (OV NZ-7).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Parapoxvirus.			
OX	NCBI_TaxID=73495;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94076465; PubMed=8254780;			
RA	Lyttle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;			
RT	"Homologs of vascular endothelial growth factor are encoded by the			
RT	poxvirus orf virus.";			
RL	J. Virol. 68:84-92(1994).			
CC	-I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; S67522; AAB29223.1; -			
DR	HSPP; P15692; IVPF.			
DR	InterPro: IPR000072; -			
DR	Pfam; PF00341; PDGF; 1.			
DR	PROSITE; PS00249; PDGF_1; FALSE_NEG.			
DR	PROSITE; PS0278; PDGF_2; 1.			
KW	Mitogen; Growth factor; Glycoprotein; Signal.			
FT	SIGNAL 1 ?			
FT	CHAIN ? 148			
FT	VASCULAR ENDOTHELIAL GROWTH FACTOR			
FT	HOMOLOG.			
FT	DISULFID 46 88			
FT	BY SIMILARITY.			
FT	DISULFID 77 130			
FT	BY SIMILARITY.			
FT	DISULFID 81 132			
FT	BY SIMILARITY.			
FT	DISULFID 71 71			
FT	INTERCHAIN (BY SIMILARITY).			
FT	DISULFID 80 80			
FT	INTERCHAIN (BY SIMILARITY).			
FT	DISULFID 95 95			
FT	N-LINKED (GLCNAC...) (POTENTIAL).			
SQ	SEQUENCE 148 AA; 16078 MW; F0E13BA104CC73F8 CRC64;			

Query Match 13.6% Score 100.5; DB 1; Length 148;
Best Local Similarity 25.6% Pred. No. 0.00082;
Matches 32; Conservative 13; Mismatches 31; Indels 49; Gaps 5;
Qy 34 CTPRNSYNIREEL-KLANVVFFPRCLLVQRCCGNCG-----CGTVNWRSC----- 79

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Db 46 CKPRDTVVYLGEEYDESTNLOYNPCVTKRCGCGNGDQICCTAVETRTNTTVTSVTCV 105
QY 80 -----CNSGKTVKKYHEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCI-----CS 127
Db 106 SSSSTGNSGVSTN-----LORISVTEHTKDCICIGRTTTTPT 142
QY 128 SRPPR 132
Db 143 TREPR 147

RESULT 2
VEGB_MOUSE
ID VEGB_MOUSE STANDARD; PRT; 188 AA.
AC P49766;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
  ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
GN VEGFB OR VRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pettefsson R.F., Alitalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells."
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96183052; PubMed=8607868;
RA Townsend S., Lagercrantz J., Grimmond S., Silins G.,
RA Nordenskjöld M., Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene."
RL Biochem. Biophys. Res. Commun. 220:922-928(1996).
CC -!- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
  WITH VEGF.
CC -!- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
  TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN HEART, BRAIN, KIDNEY
  AND SKELETAL MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U48800; AAB06273.1; -
DR EMBL; U43837; AAC52553.1; -
DR HSSP; P15692; 2VGH.
DR MGD; MGI:106199; Vegfb.
DR InterPro; IPR000072; -
DR Pfam; PF00341; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Signal; Heparin-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 188 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
SQ SEQUENCE 188 AA; 21442 MW; D52A055F995E9CA CRC64;

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Query Match 13.0%; Score 95.5; DB 1; Length 188;
Best Local Similarity 27.9%; Pred No. 0.0035;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPRNVSVNIREELKLANVY--FFPRCLLVQRCGNCGGCTVNRSCNCGTKVKK 88
Db 44 RATCQPREVVVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLCEVPTGQHOVRM 99
QY 89 YHEVLFQFEGHKKRGRKTMALVDIQLDHHERCDCICSSRPPR 132
Db 100 QILMTQY-----PSSQLGEMSEEHQSQCEC-----RPKK 128

RESULT 3
PDGA_RABIT
ID PDGA_RABIT STANDARD; PRT; 213 AA.
AC P34007;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
  (PDGF-1).
DE (PDGF-1).
GN PDGFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RX MEDLINE=92246970; PubMed=1575749;
RA Nakahara K.-I., Nishimura H., Kuro-O M., Takewaki S.-I., Iwase M.,
RA Ohkubo A., Yazaki Y., Nagai R.;
RT "Identification of three types of PDGF-A chain gene transcripts in
RT rabbit vascular smooth muscle and their regulated expression during
RT development and by angiotensin II."
RL Biochem. Biophys. Res. Commun. 184:811-818(1992).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
  CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
  AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
  RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
  IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
  AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
  TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A1, A2 (SHOWN HERE) AND A3; ARE
  PRODUCED BY ALTERNATIVE SPLICING.
CC -!- INDUCTION: THE FORM A3 IS SELECTIVELY INDUCED BY ANGIOTENSIN II.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
  PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
DR PIR; JS0735; JS0735.
DR PIR; PS0387; PS0387.
DR PIR; JN0248; JN0248.
DR HSSP; P01127; 1PDG.
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
  Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT PROPEP 21 89 REMOVED BY PROTEOLYSIS (BY SIMILARITY).
FT CHAIN 90 213 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
FT SITE 158 162 RECEPTOR-BINDING SITE (POTENTIAL).
FT DISULFID 131 179 BY SIMILARITY.
FT DISULFID 135 181 BY SIMILARITY.
FT DISULFID 125 125 INTERCHAIN (BY SIMILARITY).
FT DISULFID 134 134 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT  VARSPLIC 196 198 GRR -> DVR (IN ISOFORM A1).
FT  VARSPLIC 199 213 MISSING (IN ISOFORM A1).
FT  VARSPLIC 197 213 RRESGKKRRKRLRPT -> TLLPAGGVHPOGCLRAHDG
FT  VARSPLIC 197 213 CQSRNHMOALGWKKM (IN ISOFORM A3).
SQ  SEQUENCE 213 AA; 24005 MW; 28A9B7E50487F4C5 CRC64;

Query Match 12.8%; Score 94; DB 1; Length 213;
Best Local Similarity 28.0%; Pred. No. 0.0058;
Matches 23; Conservative 17; Mismatches 32; Indels 10; Gaps 3;

QY 50 ANVVFPRCLLVQRCGCGGTWNRSCTCNSGKTVKKYHEVLOFEPGHKRRGRAKTM 109
    || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 117 ANFLWPPCVVEVKCTGCC-----NTSVKQCPGRVHRSYKVAKE--YVRKKPKLKE- 168

QY 110 ALVDIQLDHHERCDICSSRPP 131
    || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 169 --VQVRLEEHLECAACASSAGP 188

RESULT 4
VEGC_HUMAN STANDARD; PRT; 419 AA.
AC P49767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-
DE L).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RX MEDLINE=96178224; PubMed=8617204;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RA "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
RT the FLT4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.";
RL EMBO J. 15:290-298(1996).
RN [2]
RN ERRATUM.
RX MEDLINE=96203094; PubMed=8612600;
RA Joukov V., Pajusola K., Kaipainen A., Chilov D., Lahtinen I., Kukk E.,
RA Saksela O., Kalkkinen N., Alitalo K.;
RL EMBO J. 15:1751-1751(1996).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=96312526; PubMed=8700872;
RA Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
RA "Vascular endothelial growth factor-related protein: a ligand and
RT specific activator of the tyrosine kinase receptor Flt4.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RN SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,
RA Burgess P., Giannotti J., Ciarletta A., Hennessey D., Kovacic S.,
RA Fitzgerald M., Scaltreto H., Welch N., Neben S., Finnerty H.,
RA Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K.,
RA Wood C.R.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- PTM: PROBABLY PROTEOLITICALLY PROCESSED IN THE C-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC -----
CC EMBL; X94216; CAA63907.1; -
CC EMBL; U43142; AAA85214.1; -
CC EMBL; U58111; AAB02909.1; -
CC HSP; P15692; 1VPF.
CC MIM; 601528; -
CC InterPro; IPR000072; -
CC InterPro; IPR002400; -
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS00278; PDGF_2; 1.
CC Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
KW SIGNAL 1 ?
FT PROPEP ? 102
FT CHAIN 103 419 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
FT DOMAIN 275 365 4 X 24 AA TANDEM REPEATS.
FT REPEAT 275 298 1.
FT REPEAT 299 322 2.
FT REPEAT 323 346 3.
FT REPEAT 347 365 4 (PARTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 46883 MW; 9F598719DB3E014F CRC64;

Query Match 12.6%; Score 93; DB 1; Length 419;
Best Local Similarity 20.7%; Pred. No. 0.015;
Matches 38; Conservative 20; Mismatches 50; Indels 76; Gaps 8;

QY 22 LDRLNDDAKRYSCTPRNYSVNIREELKLANVVF-PRCLLVORCGNG- 69
    | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 119 LKSIDNEWRKTCQMPREVCIDVGKEFGVATNTEFKPCVSVYRGCGCGNSEGQCMTST 178

QY 70 -----CGTVNWRSCNCSGKTV-KKYHEVLQ----- 94

Db 179 SYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVYRQVHSIIRSLPATLPQCQA 238

QY 95 -----FEPGHKIR-----RGRKTMALVDI-----QLDHHRCDCICSS 128
    || || || || || || || || || || || || || || || || || || || || ||
Db 239 ANKTCPTNYMWNHICRCLAQEDFWSDDGDDSTDFGHDICGPNKELD-EETCCQVCRA 297

QY 129 --RP 130
    ||
Db 298 GLRP 301

RESULT 5
VEGC_MOUSE STANDARD; PRT; 415 AA.
AC P97953;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FLT4 LIGAND)
DE (FLT4-L).
GN VEGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA MEDLINE=97164697; PubMed=9012504;
RA Kukk E., Lymboussaki A., Taira S., Kaipainen A., Jeltsch M.,
RA Joukov V., Alitalo K.;
RT "VEGF-C receptor binding and pattern of expression with VEGFR-3

```

RT suggests a role in lymphatic vascular development.";

RL Development 122:3829-3837(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=97388482; PubMed=9247316;

RA Fitz L.J., Morris J.C., Towler P., Long A., Burgess P., Greco R.,

RA Wang J., Gassaway R., Nickbarg E., Kovacic S., Ciarletta A.,

RA Giannotti J., Finnerty H., Zollner R., Beier D.R., Leak L.V.,

RA Turner K.J., Wood C.R.;

RT "Characterization of murine Flt4 ligand/VEGF-C.";

RL Oncogene 15:613-618(1997).

CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL

CC CELL GROWTH.

CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

CC -----

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CC -----

DR EMBL; U73620; AAC52984.1; -;

DR EMBL; U58112; AAB46707.1; -;

DR HSSP; P15692; 1VPF.

DR MGD; MGI:109124; Vegfc.

DR InterPro; IPR000072; -;

DR InterPro; IPR002400; -;

DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PROSITE; PS00249; PDGF.1; 1.

DR PROSITE; PS0278; PDGF.2; 1.

KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 ?

FT PROPEP ? 98

FT CHAIN 99 415

FT DOMAIN 271 361

FT REPEAT 271 294

FT REPEAT 295 318

FT REPEAT 319 342

FT REPEAT 343 361

FT CARBOHYD 171 171

FT CARBOHYD 201 201

FT CARBOHYD 236 236

SQ SEQUENCE 415 AA; 46471 MW; D9D3DD3CECC659D6 CRC64;

Query Match 12.5%; Score 92; DB 1; Length 415;

Best Local Similarity 24.3%; Pred. No. 0.019;

Matches 27; Conservative 18; Mismatches 42; Indels 24; Gaps 4;

QY 22 LDRLNDKAKRYCTPRNYSVNTREELKLANVVF-PRCLLVRCGNCGCCGVNWRSC7C 80

Db 115 LKSIDNEWKRTQCMPEVICDVKEFGAATNFFKPCVSVYRCGCC-----NSEGLQC 169

QY 81 NSGKTVKKYHVLQFPGGHKRRGAKTAL-----VDIQLDHHERCDCI 125

Db 170 MNTST-----GYLSKTLFEITVLSQGPVTVISFANHTSCRM 208

RESULT 6

PDGA_RAT

ID PDGA_RAT

AC P28576; STANDARD; PRT; 204 AA.

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)

DE (PDGF-1).

GN PDGPA OR RPAL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 8-204 FROM N.A.

RX MEDLINE=93305723; PubMed=8318539;

RA Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;

RT "Conservation in sequence and affinity of human and rodent PDGF

RT ligands and receptors.";

RL Biochim. Biophys. Acta 1173:294-302(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93191115; PubMed=8447423;

RA Katayose D., Ohe M., Yamauchi K., Ogata M., Shirato K., Fujita H.,

RA Shibahara S., Takishima T.;

RT "Increased expression of PDGF A- and B-chain genes in rat lungs with

RT hypoxic pulmonary hypertension.";

RL Am. J. Physiol. 264:L100-L106(1993).

RN [3]

RP SEQUENCE FROM N.A. (SHORT FORM).

RA Xia Y., Feng L., Tang W.W., Wilson C.B.;

RT "Cloning and expression of rat platelet-derived growth factor

RT A-chain.";

RL J. Am. Soc. Nephrol. 3:622-622(1992).

RN [4]

RP SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).

RC STRAIN=FISCHER 344; TISSUE=Smooth muscle;

RX MEDLINE=93225589; PubMed=8469035;

RA Szabo P., Wexler D., Whittington E., Wexler B.B.;

RT "The age-dependent proliferation of rat aortic smooth muscle cells is

RT independent of differential splicing of PDGF A-chain mRNA.";

RL Mech. Ageing Dev. 67:79-89(1993).

CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR

CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS

CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS

CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE

CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.

CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A

CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN

CC TRANSFORMATION PROCESSES.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM

CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.

CC -!- DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER

CC FORM PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM

CC BECOMES MORE PREVALENT DURING AGING.

CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE

CC PDGF RECEPTOR.

CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

CC -----

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CC -----

DR EMBL; L06894; AAB59693.1; -;

DR EMBL; Z14120; CAA78490.1; -;

DR EMBL; D10106; BAA00987.1; -;

DR EMBL; L06238; AAA1932.1; -;

DR EMBL; S57864; AAB26134.2; -;

DR HSSP; P01127; 1PDG.

DR InterPro; IPR000072; -;

DR InterPro; IPR002400; -;

DR Pfam; PF00341; PDGF; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PROSITE; PS00249; PDGF.1; 1.

DR PROSITE; PS0278; PDGF.2; 1.

KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;

KW Signal.


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DR EMBL; M19987; AAAG0046.1; JOINED.
DR EMBL; M19989; AAAG0047.1; -.
DR EMBL; M21571; AAAG0047.1; JOINED.
DR EMBL; M19984; AAAG0047.1; JOINED.
DR EMBL; M19985; AAAG0047.1; JOINED.
DR EMBL; M19986; AAAG0047.1; JOINED.
DR EMBL; M19987; AAAG0047.1; JOINED.
DR EMBL; M19988; AAAG0047.1; JOINED.
DR EMBL; M19989; AAAG0047.1; JOINED.
DR EMBL; M20078; AAAG0047.1; -.
DR PIR; A28964; PFHUG1.
DR PIR; B28964; B28964.
DR HSSP; P01127; LPDG.
DR MIM; I73430; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 132 123
FT DISULFID 132 132
FT CARBOHYD 134 134
FT VARSPIC 134 196
FT VARSPIC 197 211
FT CONFLICT 64 66
FT SEQUENCE 211 AA; 24043 MW; 48633DDE58EFA43 CRC64;

Query Match 12.1%; Score 89; DB 1; Length 211;
Best Local Similarity 26.8%; Pred. No. 0.019;
Matches 22; Conservative 18; Mismatches 32; Indels 10; Gaps 3;

QY 50 ANVVFFPRLIVQRCGCGTIVNRSCTNSGKTVKKYKHYEVLQEPGHKRRGAKTM 109
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Db 115 ANFLIWPCCVVKRKGCC-----NTSSVKQPSRVHRSVKVAKVE--YVRKKPKLKE- 166
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 110 ALVDIOLDHHERCDICSSRP 131
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 167 --VQVLEHLEACATTSINP 186
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 8
PDGA_MOUSE STANDARD; PRT; 211 AA.
AC P20033;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN)
DE (PDGF-1).
GN PDGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN-BALB/C;
RX MEDLINE=94031105; PubMed=1340209;
RA Rorsman F., Betsholtz C.;
RT "Characterization of the mouse PDGF A-chain gene. Evolutionary
RT conservation of gene structure, nucleotide sequence and alternative
RT splicing."
RL Growth Factors 6:303-313(1992).

```

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[2]
RN SEQUENCE FROM N.A. (SHORT FORM).
RC STRAIN=F9;
RX MEDLINE=90169294; PubMed=2155144;
RA Mercola M., Wang C., Kelly J., Brownlee C., Jackson-Grusby L.,
RA Stiles C., Bowen-Pope D.;
RT "Selective expression of PDGF A and its receptor during early mouse
RT embryogenesis."
RL Dev. Biol. 138:114-122(1990).
CC -!- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEALS THE WOUND.
CC -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC TRANSFORMATION PROCESSES.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
CC -!- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC PDGF RECEPTOR.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S66873; AAB28740.2; -.
CC EMBL; S66868; AAB28740.2; JOINED.
CC EMBL; S66869; AAB28740.2; JOINED.
CC EMBL; S66870; AAB28740.2; JOINED.
CC EMBL; S66871; AAB28740.2; JOINED.
CC EMBL; S66872; AAB28740.2; JOINED.
CC EMBL; S66874; AAB28741.2; -.
CC EMBL; S66869; AAB28741.2; JOINED.
CC EMBL; S66870; AAB28741.2; JOINED.
CC EMBL; S66871; AAB28741.2; JOINED.
CC EMBL; S66872; AAB28741.2; JOINED.
CC EMBL; M29464; AAA39903.1; -.
CC PIR; A37359; A37359.
CC HSSP; P01127; LPDG.
CC MGD; MGI:97527; Pdgha.
CC InterPro; IPR000072; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00341; PDGF; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00249; PDGF_1; 1.
CC PROSITE; PS0278; PDGF_2; 1.
KW Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
FT SIGNAL 1 20
FT PROPEP 21 86
FT CHAIN 87 211
FT SITE 158 162
FT DISULFID 96 140
FT DISULFID 129 177
FT DISULFID 133 179
FT DISULFID 132 123
FT DISULFID 132 132
FT CARBOHYD 134 134
FT VARSPIC 134 196
FT VARSPIC 197 211
FT CONFLICT 92 92
FT CONFLICT 174 174
FT SEQUENCE 211 AA; 24102 MW; AC4345A10ECF4B39 CRC64;

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DR InterPro: IPR002400; -
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00249; PDGF-1; 1.
DR PROSITE: PS00278; PDGF-2; 1.
DR Glycoprotein; Mitogen; Growth factor; Platelet; Alternative splicing;
KW Signal.
KW SIGNAL.
FT SIGNAL. 1 22 REMOVED BY PROTEOLYSIS.
FT PROPEP 23 91 PLATELET-DERIVED GROWTH FACTOR, A CHAIN.
FT CHAIN 92 226 BY SIMILARITY.
FT DISULFID 101 145 BY SIMILARITY.
FT DISULFID 134 182 BY SIMILARITY.
FT DISULFID 138 184 BY SIMILARITY.
FT DISULFID 128 128 INTERCHAIN (BY SIMILARITY).
FT DISULFID 137 137 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (PROBABLE).
FT VARSPIC 198 200 GFF -> DVR (IN SHORT ISOFORM).
FT VARSPIC 201 226 MISSING (IN SHORT ISOFORM).
FT CONFLICT 199 209 MISSING (IN REF. 2).
FT CONFLICT 218 218 O -> R (IN REF. 2).
FT CONFLICT 218 218 O -> R (IN REF. 2).
FT SEQUENCE 226 AA; 25719 MW; E3E724FCF67C2FB2 CRC64;

Query Match 11.3%; Score 83; DB 1; Length 226;
Best Local Similarity 26.6%; Pred. No. 0.09;
Matches 21; Conservative 18; Mismatches 30; Indels 10; Gaps

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DB 120 ANFLWPPCPVEVRKCTGCC-----NTSSVKQPSRIHRSVKVAKVE--YVRKKPKLKE- 171
| | : | | : | | | | | | | | : | | : | | : | | : | |
QY 110 ALVDIOLDHHERCDICSS 128
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DB 172 --VLVRLLEEHLCTCTANS 188
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RESULT 12
PDGB_SHEEP STANDARD; PRT; 241 AA.
ID AC PDGB_SHEEP STANDARD; PRT; 241 AA.
IC AC Q95229;
DT DT 01-NOV-1997 (Rel. 35, Created)
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DE PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
DE DE (PDGF-2).
GS GS PDGB.
OS OS Ovis aries (Sheep).
OC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC OC Bovidae; Caprinae; Ovis.
ON ON NCBI_Taxid=9940;
RX RX [1]
RN RN SEQUENCE FROM N.A.
RC RC STRAIN=TEXEL; TISSUE=Spleen;
RA Woodall C.J., Zhang Z., Watt N.J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
CC CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
CC CC AFFINITY RECEPTOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS
CC CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
CC CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
CC CC -1- SUBUNIT: ANTI-PAALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
CC CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
CC CC TRANSFORMATION PROCESSES.
CC CC -1- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
CC CC PDGF RECEPTOR.
CC CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC CC -----
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```


A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flk-1 receptor
 EMBO J. 13, 290-296, 1996

A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flk-1 receptor
 EMBO J. 13, 290-296, 1996

Query Match 12.1%; Score 89; DB 1; Length 211;
Best Local Similarity 26.8%; Pred. No. 0.11;
Matches 22; Conservative 18; Mismatches 32; Indels

Qy	64	CGNCGCGT	VN	RSCT	CNSG	KT	VK	YH	EV	LQ	FE	97
			:		:							
Db	4	CGNCGCGS	----	SC	CGN	CGG	CK	Y	SE	---	EP	30

Search completed: September 26, 2001, 15:15:59
Job time: 50 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 12.26 Seconds
(without alignments)
221.691 Million cell updates/sec

Title: US-09-662-783-4

Perfect score: 737

Sequence: 1 MYLTPRYGRSYHDKRSKV.....DIQLDHHRCDCICSSRPPR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

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- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	14.0	321	4	US-08-915-795-9
2	103	14.0	325	4	US-08-915-795-3
3	103	14.0	354	4	US-08-915-795-5
4	103	14.0	358	4	US-08-915-795-8
5	95.5	13.0	102	1	US-08-469-427A-2
6	95.5	13.0	102	2	US-08-609-443B-2
7	95.5	13.0	102	2	US-08-569-063C-2
8	95.5	13.0	133	1	US-08-469-427A-9
9	95.5	13.0	133	2	US-08-609-443B-9
10	95.5	13.0	133	2	US-08-569-063C-9
11	95.5	13.0	188	1	US-08-469-427A-5
12	95.5	13.0	188	2	US-08-609-443B-5
13	95.5	13.0	188	2	US-08-569-063C-5
14	95.5	13.0	207	2	US-08-609-443B-13
15	95.5	13.0	207	2	US-08-569-063C-13
16	94	12.8	195	1	US-08-469-427A-7
17	94	12.8	195	2	US-08-609-443B-7
18	94	12.8	195	2	US-08-569-063C-7
19	93	12.6	350	2	US-08-999-811-4
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23	93	12.6	350	4	US-08-585-895-33
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37	89	12.1	125	1	US-08-095-898-4
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41	89	12.1	126	6	5428135-4
42	89	12.1	196	1	US-08-469-427A-12
43	89	12.1	196	1	US-08-387-845-2
44	89	12.1	196	2	US-08-569-063C-22
45	89	12.1	196	2	US-08-999-811-5

ALIGNMENTS

RESULT 1
US-08-915-795-9
; Sequence 9, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-9

Query Match 14.0%; Score 103; DB 4; Length 321;
Best Local Similarity 27.0%; Pred. No. 0.00039;
Matches 34; Conservative 17; Mismatches 47; Indels 28; Gaps 6;

Qy 120 ERDCI 125
+
+
Db 158 TGCKCL 163

RESULT 3
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent NO. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. Achen

APPLICANT: Steven A. Slicker
ATTORNEY: Karl Alitalo
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeeown, Edwards & Lenahan P.L.L.C.
STREET: 1200 G Street, NW, Suite 700
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,795
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

```

QY      66 GNCGCGTVNWRSCNSGKT---VKYHEV---LQFEPGHIKRRGRAKTMALVDIQLDHH 119
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Db      144 GCC-----NEESLICMNTSTSYISKQLFEISVPLTSVP-----ELVPKVANH 166
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QY      120 ERDCI 125
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Db      187 TGCKCL 192
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RESULT 4
US-08-915-795-8

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Query Match      14.0%; Score 103; DB 4; Length 358;
Best Local Similarity 27.0%; Pred. No. 0.00045;
Matches 34; Conservative 17; Mismatches 47; Indels 28; Gaps 6;

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Db 93 RFAATFYDTETLKV-----IDEMWQRTQSPRETCEVASSELGKTTNTFFKPPCVNVRFG 148
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QY 66 GNCCGGTVNWRSCCTCNSGKT---VKKYHEV---LQFEPGHIKRRGRAKTMAVLDIQLDHH 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 GCC-----NEEGVMCMNTSTSYISKQLFETSVPLTSPV-----ELVPVKIANH 191
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 120 ERCDCI 125
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 TGCKCL 197
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-08-469-427A-2
; Sequence 2, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusola, Katrin
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREOF

```

```

; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979cp2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; US-08-469-427A-2

Query Match 13.0%; Score 95.5; DB 1: Length 102;
Best Local Similarity 27.9%; Pred. No. 0.00068;
Matches 29; Conservative 16; Mismatches 38; Indels 21

QY 31 RYSCPTPNYSNIREELKIANVY--FFPRCLLVQRCGGNGCGTVNWRSCTCNSGK
   1 : | | | | | : | | | | | : | | | | | : | | | | | : |
Db 13 RATCPQREVVPVLSNEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTQGH
   1 : | | | | | : | | | | | : | | | | | : | | | | | : |
QY 89 YHEVLQFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPFR 132
   : | : | : | : | : | : | : | : | : | : | : | : | :
Db 69 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 97
   : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 6
US-08-609-443B-2
; Sequence 2, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/419790CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
g-569-063C-2

Query Match 13.0%; Score 95.5; DB 2; Length 102;
Best Local Similarity 27.9%; Pred. No. 0.00068;
Matches 29; Conservative 16; Mismatches 38; Indels 2

[illegible]

RESULT 8
US-08-469-427A-9
; Sequence 9, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusola, Katrī
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:

NAME: Evans, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 41979cp2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-427A-9

Query Match 13.0%; Score 95.5; DB 1; Length 133;
 Best Local Similarity 27.9%; Pred. No. 0.00095;
 Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
 QY 31 RYCTPRNYSVNIREEKLNAV--FPRCLLVORCGGCGGTNNRSCCTCNSGKTVKK 88
 Db 44 RATCPREVVPLSMEL-MGNVVKQLVPSCTVVRGCG---GCCPDDGLECVPTGQHVRM 99
 QY 89 YHEVLOFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPPR 132
 Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPPK 128

RESULT 9
 US-08-609-443B-9
 Sequence 9, Application US/08609443B
 Patent No. 5840693
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569,063
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-609-443B-9

Query Match 13.0%; Score 95.5; DB 2; Length 133;
 Best Local Similarity 27.9%; Pred. No. 0.00095;
 Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;
 QY 31 RYCTPRNYSVNIREEKLNAV--FPRCLLVORCGGCGGTNNRSCCTCNSGKTVKK 88
 Db 44 RATCPREVVPLSMEL-MGNVVKQLVPSCTVVRGCG---GCCPDDGLECVPTGQHVRM 99
 QY 89 YHEVLOFEPGHIKRRGRAKTMALVDIQLDHHRCDCICSSRPPR 132
 Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPPK 128

RESULT 10
 US-08-569-063C-9
 Sequence 9, Application US/08569063C
 Patent No. 5928939
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 TITLE OF INVENTION: DNA CODING THEREFOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,063C
 FILING DATE: 06-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-063C-9

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Db   100 QILMIQY-----PSSQLGEMSLSEHSQCCEC-----RPKK 128

RESULT 12
US-08-609-443B-5
; Sequence 5, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-609-443B-5

Query Match      13.0%; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.9%; Pred. No. 0.0015;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps

Qy 31 RYCSTPRNYSYNIREELKANLV--FFPRCLLLVQRGGNCGGTVNRSCITNSGKT VKK 88
    | : | | | : | | : | | : | | | | | : | : | : | : | : | : | : | : | : |
Db 44 RATCQPREVVVPLSMEL-MGNVVQLVPSCVTYVQRCG---GCCPDGLCECTGTGHQVRM 99
    | : | | | : | | : | | : | | | | | : | : | : | : | : | : | : | : | : |

Qy 89 YHEVLQEPGCHIKRRGRAKTMALVDIQLDHHERCDCICSSRPPR 132
    ::| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCCEC-----RPKK 128

```

```

RESULT 13
US-08-569-063C-5
; Sequence 5, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-5

Query Match 13.0%; Score 95.5; DB 2; Length 188;
Best Local Similarity 27.9%; Pred. No. 0.0015;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPRNVSVNIREELKIANVV--FFPRCLLVQRCGCGCTVNWRSCTCNSGKTVKK 88
Db 44 RATCPQREVVPVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHVRM 99

QY 89 YHEVLQFEPGHKRRGAKTMAVDIQLDHERCDDICSSRRPR 132
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 14
US-08-609-443B-13
; Sequence 13, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta

```

```

; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
; US-08-609-443B-13

Query Match 13.0%; Score 95.5; DB 2; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.0017;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPRNVSVNIREELKIANVV--FFPRCLLVQRCGCGCTVNWRSCTCNSGKTVKK 88
Db 44 RATCPQREVVPVPLSMEL-MGNVVKQLVPSCVTVQRCG---GCCPDDGLECVPTGQHVRM 99

QY 89 YHEVLQFEPGHKRRGAKTMAVDIQLDHERCDDICSSRRPR 132
Db 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPKK 128

RESULT 15
US-08-569-063C-13
; Sequence 13, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23

```

```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse
;
; US-08-569-063C-13

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Query Match      13.0%; Score 95.5; DB 2; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.0017;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCPTPNYSVNIREELKLANV--FPFRCLLVQRCGNCGGTVNWRSCITNSGKTVKK 88
   | : | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db 44 RATCPREVVVPLSMEL-MGNVYKQLVPSCVTQRCG---GCCPDDGLECVPTGHOVRM 99
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 89 YHEVLQEPGPHIKRRGAKTMALVDIQLDHHRCDCICSSRPPR 132
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 100 QILMIQY-----PSSQLGENSLEHSQCEC-----RPKR 128

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Search completed: September 26, 2001, 15:16:18
Job time: 69 sec

OM of: US-09-662-783-4 to: GenEmbl:* out_format : pfs
Date: Sep 26, 2001 8:53 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2.1/USPTO_spool/US09662783/runat_26092001_152002_26232/app_query.fasta_1.190
-DB=GenEmbl -QWMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPECL=0.000 -LOOPEXT=0.000
-XGAPOP=4.500 -XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=US09662783_cgn1_1_4771 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
-WAIT -THREADS=1

Search information block:

Query: US-09-662-783-4
Query length: 132
Database: GenEmbl.*
Database sequences: 1344157
Database length: -856060004
Search time (sec): 1284.280000

score_list:

Sequence	Strd	Orig	zscore	EScore	Len	Documentation
gb_pr1:AB033832	+	737.00	1408.11	3.4e-70	1428	AB033832 Homo sapiens hSCDGF-B
gb_pat1:AX044487	+	737.00	1405.60	4.7e-70	1882	AX044487 Sequence 1 from Paten
gb_pr7:AY027518	+	737.00	1399.45	1.0e-69	3710	AY027518 Homo sapiens iris-exf
gb_pr7:AY027517	+	737.00	1399.41	1.0e-69	3729	AY027517 Homo sapiens iris-exf
gb_pr5:AF113216	+	737.00	1399.38	1.0e-69	3739	AF113216 Homo sapiens MSTP036
gb_pat1:AX044538	+	686.00	1309.17	1.1e-64	1472	AX044538 Sequence 52 from Paten
gb_pr1:AB052170	+	682.00	1301.98	2.8e-64	1386	AB052170 Rattus norvegicus rsc
gb_pat1:AX044492	+	554.00	1056.38	1.3e-50	1110	AX044492 Sequence 6 from Paten
gb_htg14:AC067870	-	409.00	730.80	1.8e-32	160345	AC067870 Homo sapiens chrom
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gb_ov:AB0324052	-	409.00	729.64	2.1e-32	182403	AC024052 Homo sapiens chrom
gb_ov:AB033829	+	338.50	635.77	3.6e-27	1675	AB033829 Gallus gallus SCDGF n
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gb_pr7:AX028032	+	328.50	620.78	2.4e-26	1035	AX028032 Sequence 3 from Paten
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gb_r01:AF286725	+	316.50	597.54	4.8e-25	1038	AF286725 Mus musculus platelet
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gb_sy:AX028065	+	260.50	501.12	1.1e-19	279	AX028065 Sequence 36 from Paten
gb_sy:AX028086	+	260.50	501.12	1.1e-19	279	AX028086 Sequence 57 from Paten
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gb_pat1:AX027969	+	218.00	419.47	4.0e-15	262	AX027969 Sequence 37 from Paten
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gb_sy:AX028066	+	218.00	419.47	4.0e-15	262	AX028066 Sequence 37 from Paten
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seq_documentation_block: 1428 bp mRNA PRI 10-FEB-2001
LOCUS AB033832 Homo sapiens hSCDGF-B mRNA for spinal cord-derived growth factor-B,
DEFINITION complete cds.
ACCESSION AB033832
VERSION AB033832.1 GI:11602807
KEYWORDS spinal cord-derived growth factor-B; SCDGF-B.
SOURCE Homo sapiens Glioma cell_line:U373MG CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
TITLE Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
SCDGF/PDGF-C/fallotet
JOURNAL Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
PUBMED 11162582
REFERENCE 2 (bases 1 to 1428)
AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
113-8602, Japan (E-mail:t-hamada@nms.ac.jp,
Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)
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BASE COUNT 403 a 335 c 359 g 331 t
ORIGIN
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|||||
17 sserLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
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1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys 17
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DEFINITION Homo sapiens iris-expressed growth factor short form (IEGF) mRNA,
complete cds, alternatively spliced.
ACCESSION  AY027518
VERSION    AY027518.1 GI:13432062
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 3710)
            Wistow,G.
            Iris-expressed Growth Factor (IEGF)
            Unpublished
REFERENCE  2 (bases 1 to 3710)
            Wistow,G.
            Direct Submission
            Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD
            20892-2740, USA
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BASE COUNT 1169 a 724 c 703 g 1114 t
ORIGIN

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|||||
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|||||
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LOCUS AY027517 3729 bp mRNA 22-MAR-2001 PRI
DEFINITION Homo sapiens iris-expressed growth factor long form (IEGF) mRNA,
complete cds, alternatively spliced.

ACCESSION AY027517

VERSION AY027517.1 GI:13432060

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3729)

AUTHORS Wistow,G.

TITLE Iris-expressed Growth Factor (IEGF)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3729)

AUTHORS Wistow,G.

TITLE Direct Submission

JOURNAL Submitted (13-FEB-2001) MSF, NEI, 6/331, NIH, Bethesda, MD

20892-2740, USA

FEATURES Location/Qualifiers

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84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
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seq_documentation_block:

LOCUS AF113216 3739 bp mRNA 12-DEC-2000 PRI
DEFINITION Homo sapiens MSTP036 mRNA, complete cds.

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ACCESSION AF113216
VERSION AF113216.1 GI:11640579
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3739)
AUTHORS Liu, B., Liu, Y.Q., Wang, X.Y., Zhao, B., Sheng, H., Zhao, X.W., Liu, S.,
Xu, Y.Y., Ye, J., Song, L., Gao, Y., Zhang, C.L., Zhang, J., Wei, Y.J.,
Cao, H.Q., Zhao, Y., Liu, L.S., Ding, J.F., Gao, R.L., Wu, Q.Y.,
Qiang, B.Q., Yuan, J.G., Liew, C.C., Zhao, M.S. and Hui, R.T.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular
Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,
Beijing 100037, P.R. China
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LOCUS AX044538 1472 bp DNA PAT 24-NOV-2000
DEFINITION Sequence 52 from Patent WO0066736.
ACCESSION AX044538
VERSION AX044538.1 GI:11343390
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1472)
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.
TITLE Growth factor homolog zvegfa
JOURNAL Patent: WO 0066736-A 52 09-NOV-2000;
Zymogenetics, Inc. (US)
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ORIGIN

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LOCUS AB052170 1386 bp mRNA ROD 10-FEB-2001
 DEFINITION Rattus norvegicus rSCDGF-B mRNA for spinal-cord derived growth factor-B, complete cds.

ACCESSION AB052170
 VERSION AB052170.1 GI:11610600

KEYWORDS Rattus norvegicus cdna to mRNA.

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (sites)

Hameda,T., Ui-Tei,K., Imaki,J. and Miyata,Y.

Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotelin

Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)

REFERENCE 2 (bases 1 to 1386)

Hameda,T., Ui-Tei,K. and Miyata,Y.

Direct Submission

TITLE Submitted (05-DEC-2000) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; Sendagi 1-1-5, Bunkyo, Tokyo 113-8602, Japan (E-mail:t-hameda@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

FEATURES Location/Qualifiers

source 1..1386

/organism="Rattus norvegicus"

/db_xref="taxon:10116"

160..1272

/gene="rSCDGF-B"

160..1272

/gene="rSCDGF-B"

/codon_start=1

/product="spinal-cord derived growth factor-B"

/protein_id="BAB18920.1"

/db_xref="GI:11610601"

/translation="MPELILVSTILVCANFCYRDTATPOSASIKALRNANLRDESN
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 EAENDICRDEVEDVESSTVVRGWCCKGHEIPPRITSRTNQIKITTFOSDDYFVAK
 PGKITYFYFDEPEAAEINWESVTSFSGVSHSPSYMDSTLRADALDKAIEFD
 TVEDLLKYPNAPQDDLENLMDTPRYRGRSHYERKSKVDLRLNDVDKRYSCYTPRN
 HSNVRLRELKLTNAVFPCLLVQRCGNGCGCTLNWKSCTCSSGKTVKKYHEVLKFE
 PGHKRGRKAKNALVDIQLDHHERCDCISSRPPR"

BASE COUNT 383 a 330 c 332 g 341 t

ORIGIN

alignment_scores:

Quality: 682.00 Length: 132

Ratio: 5.167 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 88.636

alignment_block:

US-09-662-783-4 x AB052170 ..

Align seg 1/1 to: AB052170 from: 1 to: 1386

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17.

|||||
 874 TTGTACATGGACACCCCTCGTTATAGAGCGAGGTTCATACCATGAACGAA 923
 |||||
 17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
 |||||
 924 GTCTAAAGTGGACCTGGACAGGCTCAATGATGATGTCGAAGCGTTACAGTT 973
 |||||
 34 ysthrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 974 GCACCTCCAGGAATACACTCGGTGATCTCAGGGAGGAGTTGAAGCTGACC 1023
 |||||
 51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 |||||
 1024 AACGCAGTCTTCTTCCACGATGCTCTGTGTCAGCGCTGTGTGGCAA 1073
 |||||
 67 nCysGlyCysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyL 84
 |||||
 1074 CTGTGGTTCGCGAACTCTCAACTGGAAGTCTCTGTCAGCTGACGCTCAGGGA 1123
 |||||
 84 ysthrValLysLysTyrHisGluValLeuGlnPheGluProGlyHis1le 100
 |||||
 1124 AGACAGTAAAGAAGTATCATGAGGTACTGAAGTTTGAGCCTGGACATTTC 1173
 |||||
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1174 AAAGAAGGGCAAGCTTAAGAATATGGCTCTGTGTCATATCCAGTTGGA 1223
 |||||
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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 1224 TCATCATGAGCGATGCTGATCTGCTGAGCTCAAGACCACTCGA 1269
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seq_name: gb_pat1:AX044492

seq_documentation_block:

LOCUS AX044492 1110 bp DNA PAT 24-NOV-2000

DEFINITION Sequence 6 from Patent WO00066736.

ACCESSION AX044492

VERSION AX044492.1 GI:11343347

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1110)

AUTHORS Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.

TITLE Growth factor homolog zveg4

JOURNAL Patent: WO 0066736-A 6-09-NOV-2000;

ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

source 1..1110

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="degenerate sequence"

BASE COUNT 215 a 94 c 178 g 139 t 484 others

ORIGIN

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Quality: 554.00 Length: 131

Ratio: 5.276 Gaps: 0

Percent Similarity: 80.153 Percent Identity: 74.046

alignment_block:

US-09-662-783-4 x AX044492 ..

Align seg 1/1 to: AX044492 from: 1 to: 1110

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|||||

715 ATGTAYTYNGAYACCCNMGNTAYMGNGMGNWSNTAYCAYGAYMGNA 764

|||||

17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34

|||||

765 RWSNAARGTNGAYTYNGAYMGNTNAAAYGAYGAYGCNAARMGNTAYSNT 814

34 ysthrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 815 GYACNCCMGNAAYTAYWSNGTAAATYATMGNGARGARYTNAARYTNGCN 864

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 865 AAYGTGNTNTTYYTCNMGNTGYTNTYGTGTCARMGNTGYGNGGNA 914

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 915 YTGCGTGTGGNACNCTNAATYTCGNGWNTGYACNTGYAAYWSNGNA 964

84 ysthrValLysLysTyrHisGluValLeuGluPheGluProGlyHisIle 100
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 965 ARACNGTNAARAATAYCAYGARGTNTNCARTTYGARCNGGNCAYATH 1014

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 1015 AARMGNGNGNGMGNGCNAARACNATGCGNYTNGTNGAYATHCARYTNGA 1064

117 pHisHisGluArgCysAspCysIleCysSerArgProPro 131
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seq_name: gb_htg14:AC067870

seq_documentation_block:
 LOCUS AC067870 160345 bp DNA HTG 23-JUN-2000
 DEFINITION Homo sapiens chromosome 11 clone RP11-475J2 map 11, WORKING DRAFT
 SEQUENCE, 18 unordered pieces.
 ACCESSION AC067870
 VERSION AC067870.3 GI:8671974
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 160345)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Balgwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
 Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
 Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczkv,J.,
 Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
 Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,K., O'Donnell,P.,
 O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severi,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 TITLE Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 JOURNAL On Jun 23, 2000 this sequence version replaced gi:8099852.
 COMMENT All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11"
 /clone="RP11-475J2"
 /clone_lib="RPC1-11 Human Male BAC"
 1..946
 /note="assembly_fragment
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 vector_side:right"

Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L8810
 Center clone name: 475_J2
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 151812 bases at least Q40
 Consensus quality: 156075 bases at least Q30
 Consensus quality: 157717 bases at least Q20
 Insert size: 163000; agarose-fp
 Quality coverage: 158645; sum-of-contigs
 Quality coverage: 4.9 in Q20 bases; agarose-fp
 Quality coverage: 5.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 946: contig of 946 bp in length
 947 1046: gap of 100 bp
 1047 2803: contig of 1757 bp in length
 2804 2903: gap of 100 bp
 2904 4474: contig of 1571 bp in length
 4475 4574: gap of 100 bp
 4575 8112: contig of 3538 bp in length
 8113 8212: gap of 100 bp
 8213 11442: contig of 3230 bp in length
 11443 11542: gap of 100 bp
 11543 14027: contig of 2485 bp in length
 14028 14127: gap of 100 bp
 14128 17482: contig of 3355 bp in length
 17483 17582: gap of 100 bp
 17583 20007: contig of 2425 bp in length
 20008 20107: gap of 100 bp
 20108 26548: contig of 6441 bp in length
 26549 34423: contig of 7775 bp in length
 34424 34523: gap of 100 bp
 34524 41559: contig of 7036 bp in length
 41560 41659: gap of 100 bp
 41660 50886: contig of 9227 bp in length
 50887 50986: gap of 100 bp
 50987 64203: contig of 13217 bp in length
 64204 64303: gap of 100 bp
 64304 75627: contig of 11324 bp in length
 75628 75727: gap of 100 bp
 75728 91802: contig of 16075 bp in length
 91803 91902: gap of 100 bp
 91903 110040: contig of 18138 bp in length
 110041 110140: gap of 100 bp
 110141 130770: contig of 20630 bp in length
 130771 130870: gap of 100 bp
 130871 160345: contig of 29475 bp in length.

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misc_feature 4575. 8112
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misc_feature 8213. 11442
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misc_feature 11543. 14027
/note="assembly_fragment"
misc_feature 14128. 17482
/note="assembly_fragment"
misc_feature 17383. 20007
/note="assembly_fragment"
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vector_side:right"
misc_feature 20108. 26548
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misc_feature 26649. 34423
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misc_feature 34524. 41559
/note="assembly_fragment"
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misc_feature 50987. 64203
/note="assembly_fragment"
misc_feature 64304. 75627
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misc_feature 75728. 91802
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/note="assembly_fragment"
misc_feature 110141. 130770
/note="assembly_fragment"
misc_feature 130871. 160345
/note="assembly_fragment"
BASE_COUNT 48193 a 30956 c 30439 g 49055 t 1702 others
ORIGIN

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Quality: 409.00 Length: 73
Ratio: 5.603 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-662-783-4 x AC067870/rev ..
Align seg 1/1 to reverse of: AC067870 from: 1 to: 160345

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|||||
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|||||

36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnVal 53
|||||
18947 CAGGAATTACTCGTCAATATAAGAGAAGAGCTGAAGTTGGCCAAATGTGG 18898
|||||

53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
|||||
18897 TCTTCTTCCAGCTGTCCTCCCTCGTGCAGCGCTGTGAGGAAATTTGTGC 18848
|||||

70 CysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyLysThrVa 86
|||||
18847 TGTGGAACTGTCACTGGAGGCTCTGCACATGCATTCAGGGAACCGT 18798
|||||

86 lLysLysTyrHisGluVal 92
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18797 GAAAGAGTATCATGAGGTA 18779

seq_name: gb_hcg24:AP002989
seq_documentation_block:

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LOCUS
DEFINITION
AP002989 164771 bp DNA HTG 05-DEC-2000
Homo sapiens chromosome 11 clone RP11-475J2 map 11q, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
ACCESSION
AP002989
VERSION
AP002989.1 GI:11559304
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164771)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 164,771 genomic DNA of 11q
Published Only in DataBase (2000) In press
2 (bases 1 to 164771)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (01-DEC-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gscc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
tel:81-45-503-9111, fax:81-45-503-9170)
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gscc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-475J2
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ER-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 161781 bases at least Q40
Consensus quality: 162965 bases at least Q30
Consensus quality: 163349 bases at least Q20
Insert size: 163471; sum-of-contigs
Quality coverage: 8.50x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
14 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 34180 contig of 34180 bp in length
34281 68840 contig of 34560 bp in length
68941 90300 contig of 21360 bp in length
90401 106732 contig of 16332 bp in length
106833 119529 contig of 12697 bp in length
119630 131965 contig of 12336 bp in length
132066 139832 contig of 7767 bp in length
139933 146362 contig of 6430 bp in length
146463 148684 contig of 2222 bp in length
148785 153951 contig of 5167 bp in length
154052 158926 contig of 4875 bp in length
159027 161395 contig of 2369 bp in length
161496 163230 contig of 1735 bp in length
163331 164771 contig of 1441 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 34180: contig of 34180 bp in length
* 34181 34280: gap of 100 bp

```

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* 34281 68840: contig of 34560 bp in length
* 68841 68940: gap of 100 bp
* 68941 90300: contig of 21360 bp in length
* 90301 90400: gap of 100 bp
* 90401 106732: contig of 16332 bp in length
* 106733 106832: gap of 100 bp
* 106833 119529: contig of 12697 bp in length
* 119530 119629: gap of 100 bp
* 119630 131965: contig of 12336 bp in length
* 131966 132065: gap of 100 bp
* 132066 139832: contig of 7767 bp in length
* 139833 139932: gap of 100 bp
* 139933 146362: contig of 6430 bp in length
* 146363 146462: gap of 100 bp
* 146463 148684: contig of 2222 bp in length
* 148685 148784: gap of 100 bp
* 148785 153951: contig of 5167 bp in length
* 153952 154051: gap of 100 bp
* 154052 158926: contig of 4875 bp in length
* 158927 159026: gap of 100 bp
* 159027 161395: contig of 2369 bp in length
* 161396 161495: gap of 100 bp
* 161496 163230: contig of 1735 bp in length
* 163231 163330: gap of 100 bp
* 163331 164771: contig of 1441 bp in length.
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FEATURES

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/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-475J2"
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/note="assembly_fragment"
misc_feature 68941..90300
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misc_feature 139933..146362
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misc_feature 161496..163230
/note="assembly_fragment"
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/note="assembly_fragment"
BASE COUNT 51433 a 31186 c 32085 g 48767 t 1300 others
ORIGIN
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Quality: 409.00 Length: 73
Ratio: 5.603 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AP002989/rev ..

Align seg 1/1 to reverse of: AP002989 from: 1 to: 164771

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|||||
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|||||
36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnValV 53
|||||
160335 CAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCAATGTGG 160286
|||||
53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
|||||
160285 TCCTCTTTCCACGTTGCTCTCTGTCAGCGCTGTGGAGGAATGTGGC 160236
|||||
70 CysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrVa 86
|||||
160235 TGTTGAACTGTCACTGGAGGTCTGTCACATGCAATTGAGGAAACCGT 160186
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86 lLysLysTyrHisGluVal 92
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160185 GAAAAGTATCATGAGGTA 160167
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seq_name: gb_htg24:AP003043

seq_documentation_block:

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LOCUS AP003043 180709 bp DNA HTG 14-DEC-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-617B3 map 11q, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
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ACCESSION AP003043
VERSION AP003043.1 GI:11862945
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-617B3.
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 180709)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens 180,709 genomic DNA of 11q
JOURNAL Published Only in DataBase (2000) In press
REFERENCE 2 (bases 1 to 180709)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan 305-8565, Japan
(E-mail:hattori@gs.c.riken.go.jp, URL:http://hgp.gs.c.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
```

COMMENT

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Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gs.c.riken.go.jp/
Contact: hattori@gs.c.riken.go.jp
----- Project Information
Center project name: HumDrafit1
Center clone name: RP11-617B3
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 177736 bases at least Q40
Consensus quality: 178788 bases at least Q30
Consensus quality: 179187 bases at least Q20
Insert size: 179309; sum-of-contigs
Quality coverage: 8.67x in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 34592 contig of 34592 bp in length
 34693 58129 contig of 23437 bp in length
 58230 76694 contig of 18465 bp in length
 76795 96488 contig of 19694 bp in length
 96589 110977 contig of 14389 bp in length
 111078 124491 contig of 13414 bp in length
 124592 137310 contig of 12719 bp in length
 137411 148870 contig of 11460 bp in length
 148971 156231 contig of 7261 bp in length
 156332 159291 contig of 2960 bp in length
 159392 185618 contig of 6227 bp in length
 185719 170537 contig of 4819 bp in length
 170638 175407 contig of 4770 bp in length
 175508 179193 contig of 3686 bp in length
 179294 180709 contig of 1416 bp in length.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 34592: contig of 34592 bp in length
 34693 34692: gap of 100 bp
 34693 58129: contig of 23437 bp in length
 58130 58229: gap of 100 bp
 58230 76694: contig of 18465 bp in length
 76695 76794: gap of 100 bp
 76795 96488: contig of 19694 bp in length
 96489 96588: gap of 100 bp
 96589 110977: contig of 14389 bp in length
 110978 111077: gap of 100 bp
 111078 124491: contig of 13414 bp in length
 124492 124591: gap of 100 bp
 124592 137310: contig of 12719 bp in length
 137311 137410: gap of 100 bp
 137411 148870: contig of 11460 bp in length
 148871 148970: gap of 100 bp
 148971 156231: contig of 7261 bp in length
 156232 156331: gap of 100 bp
 156332 159291: contig of 2960 bp in length
 159292 159391: gap of 100 bp
 159392 165618: contig of 6227 bp in length
 165619 165718: gap of 100 bp
 165719 170537: contig of 4819 bp in length
 170538 170637: gap of 100 bp
 170638 173407: contig of 4770 bp in length
 173408 175507: gap of 100 bp
 175508 179193: contig of 3686 bp in length
 179194 179293: gap of 100 bp
 179294 180709: contig of 1416 bp in length.

FEATURES

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 124592. .137310
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misc_feature 137411. .148870
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BASE COUNT 56284 a 33949 c 34829 g 54247 t 1400 others
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 Ratio: 5.603 Gaps: 0
 Percent Similarity: 100.000. Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AP003043/rev ..

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36 OArgAsnTyrSerValAsnIleArgGluLeuLysLeuAlaAsnVal 53
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 167047 CAGGAATTACTCGGTCAATATAGAGAAGAGCTGAAGTTGGCCCAATGTGG 166998

53 aPhePheProArgCysLeuValGlnArgCysGlyGlyAsnCysGly 69
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 166997 TCCTCTTCCAGCTGCTCCTCGTCAGCGCTGTGGAGAAATTTGGC 166948

70 CysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyLysThrVa 86
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 166947 TGTGGAACGTCAACTGGAGGCTCTGCACATGCAATTCAGGGAACCGT 166898

86 lLysLysTyrHisGluVal 92
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seq_name: gb_htg9:AC024052

seq_documentation_block:
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 DEFINITION Homo sapiens chromosome 11 clone RP11-617B3, WORKING DRAFT
 SEQUENCE, 7 unordered pieces.
 ACCESSION AC024052
 VERSION AC024052.3 GI:9838295
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 182403)
 AUTHORS Waterston,R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 182403)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

On Aug 17, 2000 this sequence version replaced gi:7109658.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0617B03
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer; plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178574 bases at least Q40
Consensus quality: 179480 bases at least Q30
Consensus quality: 179940 bases at least Q20
Insert size: 198000; agarose-fp
Insert size: 183143; sum-of-contigs
Quality coverage: 5.39 in Q20 bases; agarose-fp
Quality coverage: 5.87 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1 1666: contig of 1666 bp in length
* 1667 1766: gap of unknown length
* 1767 9133: contig of 7367 bp in length
* 9134 9233: gap of unknown length
* 9234 20663: contig of 11430 bp in length
* 20664 20763: gap of unknown length
* 20764 35927: contig of 15164 bp in length
* 35928 36028: gap of unknown length
* 36028 61610: contig of 25583 bp in length
* 61611 61710: gap of unknown length
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* 96168 96267: gap of unknown length
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36028..61610
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Quality: 409.00 Length: 73

Ratio: 5.603 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AC024052/rev ..

Align seg 1/1 to reverse of: AC024052 from: 1 to: 182403

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36 oArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAlaAsnValV 53
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154016 CAGGAATTACTCGGTCAATATAAGAGAGAGAGCTGAAGTTGGCCAATGTGG 153967
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53 alPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGly 69
|||||
153966 TCTTCTTTCCACGTTGCCTCCTCGTCGACGCTGTGGAGGAAATTTGTGGC 153917
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70 CysGlyThrValAsnTyrArgSerCysThrCysAsnSerGlyLysThrVa 86
|||||
153916 TGTGGAAGTATCATGAGGTA 153848
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86 lLysLysTyrHisGluVal 92
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seq_documentation_block:

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LOCUS AB033829 1675 bp mRNA VRT 26-JUL-2000
DEFINITION Gallus gallus SCDGF mRNA for spinal cord-derived growth factor,
complete cds.
ACCESSION AB033829
VERSION AB033829.1 GI:9392291
KEYWORDS spinal cord-derived growth factor; scdGF gene.
SOURCE Gallus gallus (strain:white leghorn) embryo spinal cord cDNA to
mRNA.

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ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

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AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE A novel gene derived from developing spinal cords, SCDGF, is a
unique member of the PDGF/VEGF family(1)
JOURNAL FEBS Lett. 475 (2), 97-102 (2000)
MEDLINE 20317014
REFERENCE 2 (bases 1 to 1675)
AUTHORS Hamada,T., Ui-Tei,K. and Miyata,Y.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-1999) to the DDBJ/EMBL/GenBank databases.
Tsuvooshi Hamada, Nippon Medical School, Department of Pharmacology;
1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan
(E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277),
Fax:81-3-5814-1684)

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FEATURES

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TLVPHHTEAPSPSLPSPALPLDLNNAVAGFTVEELIRYLEPDRWQLDLELYRP
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Ratio: 3.419 Gaps: 4
Percent Similarity: 76.744 Percent Identity: 50.388

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16 GlySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
795 AAAATCAAGAGTGGTGTGATCTCAACTTGTCTAAAGGAGGAAGTGGCTGT 844
32 YrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
845 ATAGTGTGATCTCTCCCACTTCTCAGTGTCACTGAGAGGAGGAGCTGAAG 894
49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
895 CGAACTGACACCATTTCTGGCCACTGTCTCTCTGTTAAGGCTGTGG 944
65 YGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
945 TGGAAACTGTGCTGTGTGTATCAGAACTGCAATGAGTGCATATGATAC 994
82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
995 CAAACAAGTACCAAAAAGTACCAGAGGTCTTCAGCTGAAGCCA... 1041
99 HisIleLysArgArgGly...ArgAlaLysThrMetAlaLeuValAsp11 114
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DEFINITION Sequence 3 from Patent WO0037641.
ACCESSION AX027935
VERSION AX027935.1 GI:10188752
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 3 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)

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/db_xref="taxon:9606"
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Percent Similarity: 76.562 Percent Identity: 49.219
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16 GlySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
693 AAAATCCAGAGTGGTGTGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 742
32 YrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
743 ACAGCTGCACACCTCTGTAACCTTCTCAGTGTCCATAGGAGAACTAAG 792
49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysG1 65
793 AGAACCAGATACCATTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGG 842
65 YGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
843 TGGGAACTGTGCTGTGTGTCTCCACAATTCGAATGAATGTCATGTCTCC 892
82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
893 CAAGCAAGTGTACTAAAAATACCAGAGGCTCTCTCAGTTGAGACCA... 939
99 HisIleLysArgArgGlyArgAlaLysThrMetAlaLeuValAsp1leG1 115
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VERSION AX028032.1 GI:10188844
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gordon,R.D., Dijkmans,J.J., Sprengel,J.J., Yon,J.R., Xu,J.,
Gosiewska,A. and Dhanaraj,S.N.
TITLE Vascular endothelial growth factor-x
JOURNAL Patent: WO 0037641-A 29-JUN-2000;
GORDON ROBERT DOUGLAS (BE) ; DIJKMANS JOSIENA JOHANNA HUBER (BE) ;
JANSSEN PHARMACEUTICA NV (BE) ; SPRENGEL JORG JURGEN (BE) ; YON
JEFFREY ROLAND (BE) ; XU JEAN (US) ; GOSIEWSKA ANNA (US) ; DHANARAJ
SRIDEVI NAIDU (US)
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    Ratio: 3.352      Gaps: 3
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643 CTATAAGGCCAACCTTGGCAACTCTTTGGCAAGGCTTTGTGTTTGGAG 692

16 qLysSerLys...ValAspLeuAspArgLeuAsnAspAspAlaLysArgT 32
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693 AAATCCAGAGTGGTGAATCTGAACCTTCTAACAGAGGAGGTGAAGATTAT 742

32 TyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLys 48
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743 ACAGCTGCACACCTCGTFAACTTCTCAGTGTCCATAAGGGAAGAACTAAG 792

49 LeuAlaAsnValValPhePheProArgCysLeuLeuValGlnArgCysGl 65
   :| | | | | | | | | | | | | | | | | | | | | | | |
793 AGAACCGATACCACTTTCTGGCCAGGTTGTCTCTGTGTTAAACGCTGCG 842

* 65 yGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnS 82
   :| | | | | | | | | | | | | | | | | | | | | | | |
843 TGGGAAGTGTGCTGTCTCTCCACAAATGCAATGAATGTCAATGTGTGCC 892

82 erGlyLysThrValLysLysTyrHisGluValLeuGlnPheGluProGly 98
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893 CAAGCAAAAGTTACTAAAAAATACACAGAGGTCTTCAGTTGAGACCA... 939

99 HisIleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGl 115
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940 .....AAGACCGGTGTCAGGGGATTGCACAAATCACTCACCAGCTGCG 983

115 nLeuAspHisHisGluArgCysAspCysIleCys 126
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984 CTGGAGCAGCACTGAGAGGTGTCACTGTGTGTGC 1017

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Date: Sep 26, 2001 8:56 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

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Database length: 313950809
Search time (sec): 109.920000

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/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24187 +			328.50	675.27	2776	1.2e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24186 +			328.50	675.08	2779	1.2e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24185 +			328.50	675.08	2825	1.2e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24184 +			328.50	675.03	2839	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24183 +			328.50	674.99	2849	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24182 +			328.50	674.99	2849	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24181 +			328.50	674.99	2849	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24180 +			328.50	674.99	2849	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24179 +			328.50	674.95	2858	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24178 +			328.50	674.81	2896	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24177 +			328.50	674.81	2896	1.3e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24176 +			328.50	674.12	3087	1.4e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24175 +			324.50	673.48	1474	1.5e-29

/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24197 + 1.6e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24196 + 324.50 673.03 1.6e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24195 + 324.50 663.89 5.2e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24194 + 324.50 663.89 5.2e-29
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24193 + 312.50 640.60 1.0e-27
/SIDSL1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAF24192 + 308.50 645.20 5.7e-28

seq_name: /SIDSL1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF24197

seq_documentation_block:

ID AAF24197 standard; DNA; 1110 BP.

XX

AC AAF24197;

DT 02-APR-2001 (first entry)

XX

DE Human VEGF-G coding region.

XX

KW Vascular endothelial growth factor; VEGF; cancer; cell;

KW angiogenesis; ss.

XX

OS Homo sapiens.

XX

PN WO200100878-A2.

XX

PD 04-JAN-2001.

XX

PF 29-JUN-2000; 2000WO-US18085.

XX

PR 30-JUN-1999; 99US-0343671.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Gearing DP;

XX

DR WPI; 2001-050129/06.

XX

New vascular endothelial growth factor family member used for diagnosis and treatment of deregulated cell growth e.g. cancer, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases -

Claim 1; Fig 1; 142pp; English.

The present invention relates to a vascular endothelial growth factor (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hypertrophic bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administration of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells.

Sequence 1110 BP; 328 A; 255 C; 263 G; 264 T; 0 other;

alignment_scores:

Quality: 737.00 Length: 132
Ratio: 5.583 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAF24197

Align seg 1/1 to: AAF24197 from: 1 to: 1110

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisArgLy 17
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1290 TCACCATGAACGATCGATTGTATCTGCAGCTCAAGACCACCTCGA 1335

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:AAA51541

seq_documentation_block:

ID AAA51541 standard; cDNA; 1882 BP.

XX AC AAA51541;

XX 26-SEP-2000 (first entry)

XX SEQ. ID. 36 from W00034474.

XX Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;
KW vulnery; ss.

XX OS Homo sapiens.

XX WO200034474-A2.

XX Key Location/Qualifiers

FT CDS 226..1338

FT /*tag= a

XX 15-JUN-2000.

XX 07-DEC-1999; 99WO-US28968.

XX 07-DEC-1998; 98US-0207120.

XX 06-JUL-1999; 99US-0142576.

XX 21-OCT-1999; 99US-0161653.

XX 12-NOV-1999; 99US-0165255.

XX (ZYMO) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

PI Gilbertson DG, West JW;

XX WFI; 2000-423420/36.

XX P-PSDB; AAY96864.

XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence

XX Disclosure; Page 161-164; 173pp; English.

XX Polypeptides comprising an epitope-bearing portion human or murine
CC ZVEGF3 (vascular endothelial growth factor homologue) are claimed. The
CC growth factors comprise a growth factor domain and a CUB domain (generic
CC sequence motifs are shown in AAY96859 and AAY96860). The growth factor
CC domain is characterized by an arrangement of cysteine residues and
CC beta-strands that is characteristic of the "cysteine knot" structure of
CC the platelet-derived growth factor (PDGF) family. The CUB domain shows
CC homology to CUB domains in neuropilins, human bone morphogenetic
CC protein-1, porcine seminal plasma protein, bovine acidic seminal fluid
CC protein and xenopus laevis tolloid-like protein. Structural analysis
CC homology predict that ZVEGF3 polypeptides complex with a second
CC polypeptide to form multimeric proteins. The human zvegfg3 gene has
CC mapped to chromosome 4q28.3. ZVEGF3 is useful for stimulating the growth
CC of fibroblasts or smooth muscle cells, for activating cell surface
CC PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated
CC cellular processes. ZVEGF3 is useful for regulating (post-development)
CC organ growth, regeneration and maintenance, as well as tissue
CC maintenance and repair processes. ZVEGF3 antagonists are useful for
CC treating cancer, rheumatoid arthritis, diabetic retinopathy, ischemic
CC limb disease, peripheral vascular disease, myocardial ischemia, vascular
CC intimal hyperplasia, atherosclerosis, wound healing, chronic liver
CC disease and haemangioma formation. ZVEGF3 can also be used to modulate
CC neurite growth and development of the nervous system, and for treating

CC neurodegenerative diseases.

XX

SQ Sequence 1882 BP; 566 A; 407 C; 430 G; 479 T; 0 other;

alignment_scores:

Quality: 737.00 Length: 132

Ratio: 5.583 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAA51541 ..

Align seg 1/1 to: AAA51541 from: 1 to: 1882

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17

|||||
940 ATGTATCTGGGACACCCCTCGGTATCGAGGAGGTATACCATCCAGCCGAA 989

17 sSerLysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34

|||||
990 GTCAAAAGCTTCACCTGGATAGGCTCAATGATCATGCCAAGCGTTACAGTT 1039

34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50

|||||
1040 GCACCTCCAGGAATTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 1089

51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67

|||||
1090 AATGTGGTCTTTCTTCCACGTTGCCTCTCGTGCAGCGCTGTGGAGAAA 1139

67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84

|||||
1140 TTGTGGCTGTGGAACTGTCACTGGAGGTCTGTCACATGCATTCAGGGA 1189

84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100

|||||
1190 AAACCGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCTGGCCACATC 1239

101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117

|||||
1240 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1289

117 pHisHisGluArgCysAspCysIleCysSerSerArgProProArg 132

|||||
1290 TCACCATGACGATCGATTGTATCTGCAGCTCAAGACCACCTCGA 1335

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT: AAD00737

seq_documentation_block:

ID AAD00737 standard; cDNA; 1934 BP.

XX AC AAD00737;

XX 08-SEP-2000 (first entry)

XX Human Platelet Derived Growth Factor (PDGF)-D encoding partial cDNA #2.

XX Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnery;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..969

FT /*tag= a

FT /partial

FT /product= "Human PDGF-D partial polypeptide #2"

FT /note= "5', truncated platelet derived growth factor"

XX

PN WO200027879-A1.
 XX 18-MAY-2000.
 XX 10-NOV-1999; 99WO-US26462.
 XX 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX WPI: 2000-376495/32.
 DR P-PSDB; AAY711129.
 XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX Claim 1; Fig 5; 11pp; English.
 XX The present sequence is the 5' truncated partial cDNA #2, encoding human
 CC platelet derived growth factor (PDGF)-D, formally known as Vascular
 CC Endothelial Growth Factor (VEGF)-G. It is derived from human foetal lung
 CC lamdag10 cDNA library. It belongs to the VEGF/PDGF family. It functions
 CC as an activator of proliferation, differentiation, growth and motility of
 CC cells, that express PDGF-D receptor. This sequence is useful for
 CC inhibiting the growth of tumours, that express PDGF-D. Expression of
 CC PDGF-D and its proteolytic cleavage for generating an activated truncated
 CC PDGF-D antagonist is useful for inhibiting tissue remodelling during the
 CC invasion of tumour cells into normal cells. PDGF-D may be used to treat
 CC wounds, atherosclerosis, metastasis and migration of smooth muscle cells.
 XX Sequence 1934 BP; 632 A; 366 C; 394 G; 542 T; 0 other;
 SQ

alignment_scores:
 Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAD00737 ..
 Align seg 1/1 to: AAD00737 from: 1 to: 1934
 1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLy 17
 571 ATGTATCTGGACACCCCTCGGTATCGAGGAGGTCATACCATGCCGGA 620
 17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
 621 GTCAAAAGTTGACCTGGATAGGCTCATGTATGATGCCAAGCGTTACAGTT 670
 34 ysThrProArgAsnTyrSerValAsnTleArgGluGluLeuLysLeuAla 50
 671 GCACCTCCAGGAATTTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGCC 720
 51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
 721 AAGTGTGCTCTTCTTCACCGTGGCTCTCTCGTCAGCGCTGTGAGGAAA 770
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 771 TTGTGGCTGTGGAACTGCAACTGAGAGTCTCTGCACATGCAATTCAGGGA 820

84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 821 AAACCGTGAAAAAGTATCATGAGGTATTACAGTTTGAGCCTGGCCACATC 870
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 871 AAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 920
 117 pHHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 921 TCACCATGACGATCGGATGTGTCTGTCAGCTCAAGACCATCTCGA 966
 seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT.AAD00738
 seq_documentation_block:
 ID: AAD00738 standard; cDNA; 2253 BP.
 XX
 AC AAD00738;
 XX
 DT 08-SEP-2000 (first entry)
 XX Human Platelet Derived Growth Factor (PDGF)-D encoding complete cDNA.
 DE Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnary;
 XX VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
 KW proliferative; activator; proliferation; differentiation; motility;
 KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
 KW atherosclerosis; wound; metastasis; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 CDS 176..1288
 FT /*tag= a
 FT /product= "human PDGF-D protein"
 FT /note= "Platelet derived growth factor"
 XX WO200027879-A1.
 XX 18-MAY-2000.
 XX 10-NOV-1999; 99WO-US26462.
 XX 10-NOV-1998; 98US-0107852.
 PR 28-DEC-1998; 98US-0113997.
 PR 26-AUG-1999; 99US-0150604.
 PR 04-OCT-1999; 99US-0157108.
 PR 05-OCT-1999; 99US-0157756.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;
 PI Oestman A, Heldin C;
 XX WPI: 2000-376495/32.
 DR P-PSDB; AAY711130.
 XX Novel polynucleotides encoding a novel growth factor of cells
 PT expressing a platelet-derived growth factor, useful for diagnostic and
 PT therapeutic applications, e.g. concerning cancer -
 XX Claim 1; Fig 7; 11pp; English.
 XX The present sequence is the complete cDNA encoding human platelet derived
 CC growth factor (PDGF)-D, formally known as Vascular Endothelial Growth
 CC Factor (VEGF)-G. It is derived from human foetal lung lamda g10 cDNA
 CC library. It belongs to the VEGF/PDGF family. It functions as an activator
 CC of proliferation, differentiation, growth and motility of cells, that
 CC express PDGF-D receptor. This sequence is useful for inhibiting the
 CC growth of tumours, that express PDGF-D. Expression of PDGF-D and its
 CC proteolytic cleavage for generating an activated truncated form is useful
 CC for regulating receptor binding specificity of PDGF-D. PDGF-D antagonist

CC is useful for inhibiting tissue remodelling during the invasion of
 CC tumour cells into normal cells. PDGF-D may be used to treat wounds,
 CC atherosclerosis, metastasis and migration of smooth muscle cells.
 XX
 SQ Sequence 2253 BP; 701 A; 464 C; 490 G; 598 T; 0 other;

alignment_scores:
 Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAD00738 ..
 Align seg 1/1 to: AAD00738 from: 1 to: 2253
 1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
 |||||
 890 ATGTATCTGGACACCCCTCGGTATCGAGCGAGTCCATACCATGACCGAA 939
 17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
 |||||
 940 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 989
 34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 990 GCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 1039
 51 AsnValValPheProArgCysLeuValGlnArgCysGlyGlyAs 67
 |||||
 1040 AATGTGGTCTTCTTCCACGTTGCTCGTCCGTCGAGCGCTGTGAGGAAA 1089
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 1090 TTGTGGCTGTGGAAGTCACTGAGGTCCTGCACATGCAATTCAGGGA 1139
 84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 |||||
 1140 AAACCGTGAAAAGATATCATGAGGTATTACAGTTTGAGCCTGCCACATC 1189
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1190 AAGAGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1239
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 1240 TCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCCACCTCGA 1285

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF24196

seq_documentation_block:

ID AAF24196 standard; DNA; 3853 BP.

AC AAF24196;

DT 02-APR-2001 (first entry)

DE Human VEGF-G cDNA.

XX Vascular endothelial growth factor; VEGF; cancer; cell;
 KW angiogenesis; ss.
 XX

OS Homo sapiens.

PN WO200100878-A2.

XX

PD 04-JAN-2001.

XX

PF 29-JUN-2000; 2000WO-US18085.

XX

PR 30-JUN-1999; 99US-0343671.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX Gearing DP;

XX WPI; 2001-050129/06.

XX New vascular endothelial growth factor family member used for diagnosis
 PT and treatment of deregulated cell growth e.g. cancer, disorders
 PT involving aberrant angiogenesis e.g. psoriasis, and chronic
 XX inflammatory diseases -

PS Claim 1; Fig 1; 142pp; English.

XX
 CC The present invention relates to a vascular endothelial growth factor
 CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid
 CC molecules are used as modulating agents or as targets for
 CC developing modulating agents to regulate a variety of cellular
 CC processes e.g. cell proliferation, differentiation, migration and
 CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,
 CC peptidomimetic or nucleic acid are used to treat a subject with
 CC aberrant VEGF-G protein or nucleic acid expression or activity
 CC e.g. deregulated cell growth, such as cancer, hyperproliferative bone
 CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,
 CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G
 CC gene expression is inhibited through the administration of antisense
 CC molecules or ribozymes and by targeting the regulatory region of VEGF-G
 CC to prevent transcription of the gene in target cells.

SQ Sequence 3853 BP; 1194 A; 771 C; 757 G; 1131 T; 0 other;

alignment_scores:

Quality: 737.00 Length: 132
 Ratio: 5.583 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-662-783-4 x AAF24196 ..

Align seg 1/1 to: AAF24196 from: 1 to: 3853

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
 |||||
 927 ATGTATCTGGACACCCCTCGGTATCGAGCGAGTCCATACCATGACCGAA 976
 17 sSerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyrSerC 34
 |||||
 977 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTACAGTT 1026
 34 ysThrProArgAsnTyrSerValAsnIleArgGluGluLeuLysLeuAla 50
 |||||
 1027 GCACCTCCAGGAATTTACTCGGTCAATATAAGAGAGAGCTGAAGTTGGCC 1076
 51 AsnValValPheProArgCysLeuValGlnArgCysGlyGlyAs 67
 |||||
 1077 AATGTGGTCTTCTTCCACGTTGCTCGTCCGTCGAGCGCTGTGAGGAAA 1126
 67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
 |||||
 1127 TTGTGGCTGTGGAAGTCACTGAGGTCCTGCACATGCAATTCAGGGA 1176
 84 ysThrValLysLysTyrHisGluValLeuGlnPheGluProGlyHisIle 100
 |||||
 1177 AAACCGTGAAAAGATATCATGAGGTATTACAGTTTGAGCCTGCCACATC 1226
 101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
 |||||
 1227 AAGAGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCAGTTGGA 1276
 117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
 |||||
 1277 TCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCCACCTCGA 1322

DR P-PSDB; AAB48663.
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease.
XX
XX Example 19; Page 136-138; 143pp; English.
PS
XX The invention relates to the human growth factor homologue zvegfg
CC (AAB48653), and nucleic acids encoding it (AAC81555). zvegfg is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. zvegfg has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. zvegfg has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegfg or fragments thereof, particularly human zvegfg4/human zvegfg3
CC fusions; expression constructs and host cells comprising human zvegfg
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
CC which binds to human zvegfg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegfg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegfg4 gene of a patient. zvegfg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells; which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents DNA encoding mouse
CC zvegfg4.
XX
XX Sequence 1472 BP; 434 A; 327 C; 332 G; 379 T; 0 other;

alignment_scores:
Quality: 686.00 Length: 132
Ratio: 5.197 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.152

alignment_block:
US-09-662-783-4 x AAC81596 ..
Align seg 1/1 to: AAC81596 from: 1 to: 1472

1 MetTyrLeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgly 17
807 TTGTATCTGGACACCCCTCATTATAGAGCAGGTGCATACCATGATCGGAA 856
17 sSerTysValAspLeuAspArgLeuAsnAspAlaLysArgTyrSerC 34
857 GTCCAAAGTGGACCTGGACAGGCTCAATCATGTCATGTCAGCTTACAGTT 906
34 yThrProArgAsnTyrSerValAsnIleArgGluLeuLeuLysLeuAla 50
907 GCACCTCCCAAGGAATCACTGTGTGAACCTCAGGAGGAGCTGAAGCTGACC 956
51 AsnValValPhePheProArgCysLeuLeuValGlnArgCysGlyGlyAs 67
957 AATGCAGCTCTTCTCCACAGATGCCCTCCCTGCGACGCTGTGGTGCAA 1006
67 nCysGlyCysGlyThrValAsnTrpArgSerCysThrCysAsnSerGlyL 84
1007 CTGTGGTTCGGAACACTGTCACTGAAGTCTCTGCACATCAGCTCAGGGA 1056
84 yThrValLysTyrTyrHisGluValLeuGlnPheGluProGlyHisIle 100
|||||

1057 AGACAGTGAAGAAGTATCATGAGGTATTCAAGTTTGAGCCTGGACATTTC 1106
101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
|||||
1107 AAGAAGGGGCAAGCTAAGAATATGCTCTTGTGTATCCAGCTGGA 1156
117 phisHisGluArgCysAspCysIleCysSerSerArgProProArg 132
|||||
1157 TCATCATGAGCGATGCTACTGTATCTATGTCAGCTCAAGACCACTCGA 1202
seq_name: /SIDS1/gcdata/geneseq/geneseqn/NA2001.DAT:AAF24199
seq_documentation_block:
ID AAF24199 standard; DNA; 1110 BP.
XX
AC AAF24199;
XX
DT 02-APR-2001 (first entry)
XX Human VEGF-G coding region.
DE
XX Human VEGF-G coding region.
KW Vascular endothelial growth factor; VEGF; cancer; cell;
KW angiogenesis; ss.
XX Homo sapiens.
OS
XX WO200100878-A2.
PN
XX
PD 04-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-US18085.
PF
XX
PR 30-JUN-1999; 99US-0343671.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Gearing DP;
PI
XX
XX WPI; 2001-050129/06.
DR
XX New vascular endothelial growth factor family member used for diagnosis
PT and treatment of deregulated cell growth e.g. cancer, disorders
PT involving aberrant angiogenesis e.g. psoriasis, and chronic
PT inflammatory diseases -
XX
XX Claim 1; Fig 8; 142pp; English.
PS
XX The present invention relates to a vascular endothelial growth factor
CC (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid
CC molecules are used as modulating agents or as targets for
CC developing modulating agents to regulate a variety of cellular
CC processes e.g. cell proliferation, differentiation, migration and
CC wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide,
CC peptidomimetic or nucleic acid are used to treat a subject with
CC aberrant VEGF-G protein or nucleic acid expression or activity
CC e.g. deregulated cell growth, such as cancer, hypertrophic bone
CC disorders, disorders involving aberrant angiogenesis e.g. psoriasis,
CC and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G
CC gene expression is inhibited through the administration of antisense
CC molecules or ribozymes and by targeting the regulatory region of VEGF-G
CC to prevent transcription of the gene in target cells.
XX
SQ Sequence 1110 BP; 313 A; 267 C; 269 G; 261 T; 0 other;

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Quality: 681.00 Length: 132
Ratio: 5.198 Gaps: 0
Percent Similarity: 99.242 Percent Identity: 89.394

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51 AsnValValPhePheProArgCysLeuValGlnArgCysGlyGlyAs 67
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117 pHISHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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AC AAF24198;
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DT 02-APR-2001 (first entry)
XX
DE Human VEGF-G cDNA.
XX
KW Vascular endothelial growth factor; VEGF; cancer; cell;
KW angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200100878-A2.
XX
PD '04-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-US18085.
XX
PR 30-JUN-1999; 99US-0343671.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Gearing DP;
XX
WPI; 2001-050129/06.
XX

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New vascular endothelial growth factor family member used for diagnosis and treatment of deregulated cell growth e.g. cancer, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases -

Claim 1; Fig 8; 142pp; English.

The present invention relates to a vascular endothelial growth factor (VEGF) family member, VEGF-G. VEGF-G protein and nucleic acid

CC molecules are used as modulating agents or as targets for developing modulating agents to regulate a variety of cellular processes e.g. cell proliferation, differentiation, migration and wound repair. VEGF-G modulators, i.e. VEGF-G protein, peptide, peptidomimetic or nucleic acid are used to treat a subject with aberrant VEGF-G protein or nucleic acid expression or activity e.g. deregulated cell growth, such as cancer, hyperproliferic bone disorders, disorders involving aberrant angiogenesis e.g. psoriasis, and chronic inflammatory diseases e.g. rheumatoid arthritis. VEGF-G gene expression is inhibited through the administration of antisense molecules or ribozymes and by targeting the regulatory region of VEGF-G to prevent transcription of the gene in target cells.

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SQ Sequence 3121 BP; 980 A; 611 C; 637 G; 893 T; 0 other;

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Percent Similarity: 99.242 Percent Identity: 89.394

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Align seg 1/1 to: AAF24198 from: 1 to: 3121

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1129 AGACAGTGAAGAAGTATCACAGAGTATTGAAGTTGAGCCTGGACATTC 1178
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101 LysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeuAs 117
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1179 AAGAGAGGGGCAAGCTAGAGAATAGCCCTCTTGTGATATCCAGCTGGA 1228
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117 pHISHisGluArgCysAspCysIleCysSerSerArgProProArg 132
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seq_name: /SIDS1/gcqdta/geneseq/geneseq/NA2000.DAT:AAC81556

seq_documentation_block:
ID AAC81556 standard; DNA; 1110 BP.

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AC AAC81556;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human growth factor homologue zveg4 degenerate DNA, SEQ ID NO:6.
XX
KW Human; zveg4; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;


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56  ProArgCysLeuValGlnArgCysGlyGlyAsnCysGlyGlyTh 72
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72  rValAsnTrpArgSerCysThrCysAsnSerGlyLysThr.....V 86
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100  IleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLe 116
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seq documentation block:
; Sequence 6, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1325 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Mouse Lung
US-08-915-795-6

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  Percent Similarity: 49.206  Percent Identity: 26.984

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23  parLeuAsnAspAlaLysArgTyrSerCysThrProArgAsnTyrS 40
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400  ...ATAGATGAAGATGGCAGAGGACCCAAATGCAGCCCTAGAGACAT 445
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56  ProArgCysLeuValGlnArgCysGlyGlyAsnCysGlyGlyTh 72
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72  rValAsnTrpArgSerCysThrCysAsnSerGlyLysThr.....V 86
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seq documentation block:
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; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,795
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269

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; REFERENCE/DOCKET NUMBER: 1064/42983
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Human Lung
; US-08-915-795-4

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  Ratio: 1.661        Gaps: 6
  Percent Similarity: 49.206      Percent Identity: 27.778

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  Align seg 1/1 to: US-08-915-795-4 from: 1 to: 2029

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672 AGGTTTGGCGCAACTTCTATGACATTGAACACATAAAAGTT..... 713

23 pArgLeuAsnAspAspAlaLysArgTyrSerCysThrProArgAsnTyrS 40
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40 erValAsnIleArgGluGluLeu...LysLeuAlaAsnValValPhePhe 55
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56 ProArgCysLeuLeuValGlnArgCysGlyGlyAsnCysGlyCysGlyTh 72
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810 CCCCCTTGTTGTAACGCTGTCGATGCTGGCTGTTGC..... 848

72 rValAsnTrpArgSerCysThrCysAsnSerGlyLysThr.....V 86
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849 ....AATGAAGAGAGCTTATCTGTATGACACACACACCTCGTACATT 894

86 alLysLysTyrHisGluVal.....LeuGlnPheGluProGlyHis 99
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895 CCAACAGCTCTTTGAGATATCAGTCGCTTGACATCAGTACCT..... 938

100 IleLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLe 116
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116 uAspHisHisGluArgCysAspCysIle 125
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959 TGCCATCATACAGGTTGTAAGTGCCTTG 986

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seq_documentation_block:
; Sequence 1, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Kari ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
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230 AGCGTGTGGT.....GGCTGCTCCCTCAGCATGGCGCTGAATGT 270
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271 GTGCCACTGGGCAACACCAAGTCCGAATCCAGATCCTCATGATCCAGTA 320
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeu 112
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321 C.....CCGAGCAGTCAGCTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysIleCysSer 128
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338 GGGAGATGTCCTGGGAAGACACAGCCCAATGTGAATGC..... 375
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; Sequence 8, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/POCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
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; TOPOLOGY: linear
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; PS-08-609-443B-8

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183 C...ATGGCAATGGTCAACACACTAGTCCAGCTGTGTGACTGTGC 229
62 InArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
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79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
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95 egluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
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321 C.....CCGACGACGTGCTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysLeuSer 128
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seq_documentation_block:
; Sequence 8, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
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; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-569-063C-8

alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
  Percent Similarity: 52.885      Percent Identity: 27.885

alignment_block:
US-09-662-783-4 x US-08-569-063C-8 ..
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31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu 47
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133 CGTGCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAAT 182
47 utylsLeuAlaAsnVal.....PhePheProArgCysLeuLeuValG 62
| : : : : : : : : : : : : : : : : : : : : : : : : :
183 C...ATGGCAATGGTCAACACACTAGTCCAGCTGTGTGACTGTGC 229
62 InArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
||||| :||||| :||||| :||| :||| :||| :||| :||| :|||
230 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCCTGGAATGT 270
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
: : : : : : : : : : : : : : : : : : : : : : : : :
271 GTGCCACTGGGCACACCAAGTCCGAATGCAGATCCTCATGATCCAGTA 320
95 egluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
: : : : : : : : : : : : : : : : : : : : : : : : :
321 C.....CCGACGACGTGCTGG 337
112 alaSpIleGlnLeuAspHisHisGluArgCysAspCysLeuSer 128
: : : : : : : : : : : : : : : : : : : : : : : : :
338 GGGAGATGTCCTGGGAAGAACACAGCAATGTGAATGC.....375

129 ArgProProArg 132
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376 AGACCAAAAAA 387

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-469-427A-4

seq_documentation_block:
; Sequence 4, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
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; Sequence 4, Application US/08609443B
; Patent NO. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-609-443B-4

alignment_scores:
    Quality: 95.50      Length: 104
    Ratio: 1.736        Gaps: 5
    Percent Similarity: 52.885    Percent Identity: 27.885

alignment_block:
US-09-662-783-4 x US-08-609-443B-4 ..

Align seg 1/1 to: US-08-609-443B-4 from: 1 to: 565

31 ArgTyrSerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu 47
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128 CGTGCACATGCCGCCCGAGGGAGTGGTGGCTCTGACCATGGAAGT 177
|||||.....|

47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
|||||.....|
178 C.....ATGGCAATGTGGTCAACAACTAGTGCACAGCTGTGTGACTGTGC 224
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62 lnArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
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225 AGCGTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 265
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79 ThrCysAsnSerGlyThrValLysLysTyrHisGluValLeuGlnPh 95
   :::::
266 GTGCCCACTGGCCACACCAAGTCGAATGCATCCATGATCCAGTA 315
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95 eGluProGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeuV 112
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316 C.....CGGACGCTCAGCTGG 332
112 alAspIleGlnLeuAspHisGluArgCysAspCysSerser 128
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333 GGGAGATGCTCCCTGGAAGAACAACAGCAATGTGAATGC..... 370
129 ArgProProArg 132
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371 AGACCAAAAAA 382

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-569-063C-4

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seq_documentation_block:
; Sequence 4, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-4

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alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
  Percent Similarity: 52.885  Percent Identity: 27.885

alignment_block:
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128 CGTGCACATGCCAGCCAGGAGGTGGTGGCTCTGAGCATGGAACT 177
   |||
47 ulysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
   |
178 C...ATGGCAATGGTCAAAACACTAGTCCACAGCTGTGTGACTGTGC 224
   |||||
62 lnArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
   |||||
225 AGCGTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 265
   |||||
79 ThrCysAsnSerGlyThrValLysLysTyrHisGluValLeuGlnPh 95
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266 GTGCCCACTGGCCACACCAAGTCGAATGCATCCATGATCCAGTA 315
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95 eGluProGlyHisIleLysArgGlyArgAlaLysThrMetAlaLeuV 112
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112 alAspIleGlnLeuAspHisGluArgCysAspCysSerser 128
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333 GGGAGATGCTCCCTGGAAGAACAACAGCAATGTGAATGC..... 370
129 ArgProProArg 132
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371 AGACCAAAAAA 382

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-609-443B-12

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seq_documentation_block:
; Sequence 12, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427

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/ FILING DATE: 06-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/569,063
/ FILING DATE: 06-DEC-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: EVANS, Joseph D
/ REGISTRATION NUMBER: 26,269
/ REFERENCE/DOCKET NUMBER: 1064/41979CP4
/ TELEPHONE: (202) 628-8800
/ TELEFAX: (202) 628-8844
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 624 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ TISSUE TYPE: mouse
/ US-08-609-443B-12
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alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
Percent Similarity: 52.885 Percent Identity: 27.885
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alignment_block:
US-09-662-783-4 x US-08-609-443B-12 ..
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Align seg 1/1 to: US-08-609-443B-12 from: 1 to: 624

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47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
180 C...ATGGGCAATGGTGTCAACAACATAGTCCCGAGCTGTGTGACTGTGC 226
62 lnArgCysGlyGlyAsnCysGlyThrValAsnTrpArgSerCys 78
227 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 267
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
268 GTGCCACTGGGCAACCAAGTCCGATGCAGATCCTCATGATCCAGTA 317
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
318 C.....CCGAGCAGTCAGCTGG 334
112 alAspIleGlnLeuAspHisHisGluArgCysAspCysIleCysSerSer 128
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129 ArgProProArg 132
373 AGACCAAAAAA 384
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-569-063C-12

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seq_documentation_block:
/ Sequence 12, Application US/08569063C
/ Patent No. 5928939
/ GENERAL INFORMATION:
/ APPLICANT: ERIKSSON, Ulf
/ APPLICANT: OLOFSSON, Birgitta
/ APPLICANT: ALITALO, Kari
/ APPLICANT: PAJUSOLA, Katri
/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
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/ TITLE OF INVENTION: DNA CODING THEREFOR
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
/ STREET: 1200 G Street, N.W., Suite 700
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/569,063C
/ FILING DATE: 06-DEC-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/469,427
/ FILING DATE: 06-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/397,651
/ FILING DATE: 01-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: EVANS, Joseph D
/ REGISTRATION NUMBER: 26,269
/ REFERENCE/DOCKET NUMBER: 1064/41979CP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-8800
/ TELEFAX: (202) 628-8844
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 624 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ TISSUE TYPE: mouse
/ US-08-569-063C-12
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alignment_scores:
  Quality: 95.50      Length: 104
  Ratio: 1.736       Gaps: 5
Percent Similarity: 52.885 Percent Identity: 27.885
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alignment_block:
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Align seg 1/1 to: US-08-569-063C-12 from: 1 to: 624

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47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
180 C...ATGGGCAATGGTGTCAACAACATAGTCCCGAGCTGTGTGACTGTGC 226
62 lnArgCysGlyGlyAsnCysGlyThrValAsnTrpArgSerCys 78
227 AGCGCTGTGGT.....GGCTGCTGCCCTGACGATGGCTGGAATGT 267
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuGlnPh 95
268 GTGCCACTGGGCAACCAAGTCCGATGCAGATCCTCATGATCCAGTA 317
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetAlaLeuV 112
318 C.....CCGAGCAGTCAGCTGG 334
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39 CGTGCCCATGCGCCAGCCAGGAGGTGGTGGCTGCTGAGCATGGAACT 88
47 uLysLeuAlaAsnValVal.....PhePheProArgCysLeuLeuValG 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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62 lnArgCysGlyAsnCysGlyCysGlyThrValAsnTrpArgSerCys 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 AGCGCTGTGGT.....GGCTGCTGCCTGACGATGCCTGGAATGT 176
79 ThrCysAsnSerGlyLysThrValLysLysTyrHisGluValLeuInPh 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 GTGCCCATGGGCACACCAAGTCCGAATGCAGATCCTCATGATCCAGTA 226
95 eGluProGlyHisIleLysArgArgGlyArgAlaLysThrMetalLeuV 112
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227 C.....CCGAGCAGTCAGCTGG 243
112 alAspIleGlnLeuAspHisHisGluArgCysAspCysIleCysSerSer 128
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244 GGGAGATGTCCCTGGAAGAACAACAGCAATGTGAATGC..... 281
129 ArgProProArg 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
282 AGACCAAAAAA 293
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-609-443B-1
seq_documentation_block:
; Sequence 1, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 22.55 Seconds
(without alignments)
774.468 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLTPRYGRSYHDKRSK.....DIQLDHERCDCICSSRP 132

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Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-unclassified.*
13: sp-vertebrate.*
14: sp-virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	370	4 Q9GZP0	Q9gqp0 homo sapien
2	682	92.5	370	11 Q9EQT1	Q9eqt1 rattus norv
3	338.5	45.9	345	13 Q9I946	Q9i946 gallus gall
4	328.5	44.6	345	4 Q9UL22	Q9ul22 homo sapien
5	328.5	44.6	345	4 Q9NR41	Q9nr41 homo sapien
6	324.5	44.0	345	11 Q9QX71	Q9qx71 mus muscucu
7	322.5	43.8	345	11 Q9EQX6	Q9eqx6 rattus norv
8	316.5	42.9	345	11 Q9JHV8	Q9jvh8 mus muscucu
9	107	14.5	326	11 Q35251	Q35251 rattus norv
10	103	14.0	354	4 Q43915	Q43915 homo sapien
11	103	14.0	358	11 P97946	P97946 mus muscucu
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13	97	13.2	304	5 Q9N413	Q9n413 caenorhabdi
14	95.5	13.0	207	11 Q64290	Q64290 mus muscucu
15	89	12.1	418	13 Q57352	Q57352 coturnix co
16	88.5	12.0	301	5 Q9WPF6	Q9wpe6 drosophila
17	88	11.9	149	11 Q9WQV7	Q9wqv7 mesocricetu
18	87.5	11.9	195	13 Q9DE50	Q9de50 brachydanio
19	87	11.8	420	6 Q9XS50	Q9xs50 bos taurus

20	86.5	11.7	188	6 Q9XS48	Q9xs48 bos taurus
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22	85.5	11.6	79	10 Q9FQ79	Q9fq79 musa acumin
23	85.5	11.6	132	14 Q9YMF3	Q9ymf3 orf virus.
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25	85	11.5	144	13 Q73822	Q73822 brachydanio
26	85	11.5	148	13 Q42571	Q42571 xenopus lae
27	85	11.5	186	5 Q9VM43	Q9vm43 xrosophila
28	85	11.5	188	13 Q73682	Q73682 brachydanio
29	85	11.5	194	13 Q42572	Q42572 xenopus lae
30	83.5	11.3	80	10 Q04107	Q04107 oryza sativ
31	80.5	10.9	341	5 Q9VX49	Q9vy49 drosophila
32	78.5	10.7	80	10 Q22488	Q22488 oryza sativ
33	78.5	10.7	334	5 Q26567	Q26567 schistosoma
34	78.5	10.7	342	5 Q26568	Q26568 schistosoma
35	78.5	10.7	366	5 Q26569	Q26569 schistosoma
36	78.5	10.7	1717	5 Q26566	Q26566 schistosoma
37	78	10.6	211	13 Q9PUF7	Q9puf7 gallus gall
38	78	10.6	297	2 Q83892	Q83892 treponema p
39	77.5	10.5	77	10 Q9ZNT5	Q9znt5 eichhornia
40	77	10.4	79	10 Q9ZRV0	Q9zrv0 fagus sylv
41	77	10.4	118	6 Q9MZB1	Q9mzb1 ovis aries
42	77	10.4	190	6 Q77643	Q77643 ovis aries
43	77	10.4	210	6 Q29613	Q29613 felis silve
44	76.5	10.4	76	10 Q9LEF4	Q9lef4 posidonia o
45	76.5	10.4	77	10 Q9SMG3	Q9smg3 eichhornia

ALIGNMENTS

RESULT 1					
Q9GZP0					
ID Q9GZP0	PRELIMINARY;	PRT;	370 AA.		
AC Q9GZP0;					
DT 01-MAR-2001	(TREMBLrel. 16, Created)				
DT 01-MAR-2001	(TREMBLrel. 16, Last sequence update)				
DT 01-MAR-2001	(TREMBLrel. 16, Last annotation update)				
DE SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036).					
GN HSCDGF-B.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OC NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Hamada T., Uti-rei K., Imaki J., Miyata Y.;					
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to					
RT SCDGF/PDGF-C/fallotein."					
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE=AORTA;					
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,					
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,					
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,					
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;					
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AB033832; BAB18903.1; -					
DR EMBL; AF113216; AAC39287.1; -					
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;					

Query Match	100.0%	Score 737;	DB 4;	Length 370;
Best Local Similarity	100.0%	Pred. No. 3.5e-74;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	MYLTPRYGRSYHDKRSKVDLRLNDKAKRYSCPTPRNSYNIREELKLANVFPRLCL 60			
Db 239	MYLTPRYGRSYHDKRSKVDLRLNDKAKRYSCPTPRNSYNIREELKLANVFPRLCL 298			
Qy 61	VORCGNCGCCTVNNRSCNTSGTKVKKYHEVLOPEPGHKRRGAKTMALVDQLDHHH 120			

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Db 299 VORCGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHE 358
QY 121 RDCICSSRRPR 132
Db 359 RDCICSSRRPR 370

RESULT 2
ID Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL-CORD DERIVED GROWTH FACTOR-B.
GN RSCDGF-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDFG/PDGF-C/fallotein.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
DR EMBL; AB052170; BAB18920.1; -.
SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;

Query Match 92.5%; Score 682; DB 11; Length 370;
Best Local Similarity 88.6%; Pred. No. 4.8e-68;
Matches 117; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 MYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCITPRNYSVNIREEKLNAVFFPRCLL 60
Db 239 LYMDTPRYGRSYHERKSKVDDRLNDLVKRYSCITPRNHSVNIREEKLNAVFFPRCLL 298

QY 61 VORCGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHE 120
Db 299 VORCGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLDHE 358

QY 121 RDCICSSRRPR 132
Db 359 RDCICSSRRPR 370

RESULT 3
Q91946 PRELIMINARY; PRT; 345 AA.
AC Q91946;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL-CORD-DERIVED GROWTH FACTOR.
GN SCDFG.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WHITE LEGHORN; TISSUE=SPINAL CORD;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; CUB; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 44.6%; Score 328.5; DB 4; Length 345;
Best Local Similarity 49.2%; Pred. No. 1.2e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;

QY 1 MYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCITPRNYSVNIREEKLNAVFFPRC 58
Db 215 LYRPTWQLLGKAYFVGRKSRVVDLNLTEVRLYSTPFRNFSVIRELKRTDTIEWPLC 274

QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 118
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DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 45.9%; Score 338.5; DB 13; Length 345;
Best Local Similarity 50.4%; Pred. No. 8.9e-30;
Matches 65; Conservative 21; Mismatches 36; Indels 7; Gaps 4;

QY 1 MYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCITPRNYSVNIREEKLNAVFFPRC 58
Db 215 LYRPTWQLLGKAYFVGRKSRVVDLNLTEVRLYSTPFRNFSVIRELKRTDTIEWPLC 274

QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 117
Db 275 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 330

QY 118 HHERCDIC 126
Db 331 HHEECDCVC 339

RESULT 4
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
DE GROWTH FACTOR).
GN HSCDGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Fallotein, a novel growth factor like gene identified in human
RT uterus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDF, is a unique
RT member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102(2000).
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; PDGF; 1.
DR Pfam; PF00341; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 44.6%; Score 328.5; DB 4; Length 345;
Best Local Similarity 49.2%; Pred. No. 1.2e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;

QY 1 MYLDTPRYGRSY-HDRKSK-VDLRLNDDAKRYSCITPRNYSVNIREEKLNAVFFPRC 58
Db 215 LYRPTWQLLGKAYFVGRKSRVVDLNLTEVRLYSTPFRNFSVIRELKRTDTIEWPLC 274

QY 59 LLVQRCGGNCGGTNNRSCNCGTKVKKYHEVLQFEPGHIKRRGRKTMALVDIQLD 118
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Db 275 LLVRCGCGNACCLHNCNECQVPSKVKYHEVLQLRP---KTGVRGLHKS LTDVALEH 331
Qy 119 HERCDCIC 126
Db 332 HEEDCVC 339
RESULT 5
Q9NRA1
ID Q9NRA1 PRELIMINARY; PRT; 345 AA.
AC Q9NRA1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
RA Betscholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
RT "PDGF-C is a novel protease-activated ligand for the PDGF alpha
RT receptor";
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL; AF244813; AAF80597.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00341; PDGF. 1.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 44.6%; Score 328.5; DB 4; Length 345;
Best Local Similarity 49.2%; Pred. No. 1.2e-28;
Matches 63; Conservative 20; Mismatches 40; Indels 5; Gaps 3;
Qy 1 MYLDTPRYGRSY-HDRKSK-VLDRLNDADAKRYSCPTPRNSVNTREELKLANVVFPRC 58
Db 215 LYRPTWQLGKAFYGRKSRVVDLNLLEEVRLYSCPTPRNSVNTREELKRTDTIFWPGC 274
Qy 59 LLVRCGCGCGGTNNWRSCTNSGKTVKHYEVLPQEPGHKRRGRKTMALVDIQLDH 118
Db 275 LLVRCGCGNACCLHNCNECQVPSKVKYHEVLQLRP---KTGVRGLHKS LTDVALEH 331
Qy 119 HERCDCIC 126
Db 332 HEEDCVC 339
RESULT 6
Q9QY71
ID Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FALLOTEIN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;

"cDNA cloning of follotein from mouse ovary";
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF117608; AAE22516.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
Query Match 44.0%; Score 324.5; DB 11; Length 345;
Best Local Similarity 48.4%; Pred. No. 3.3e-28;
Matches 62; Conservative 22; Mismatches 39; Indels 5; Gaps 3;
Qy 1 MYLDTPRYGRSY-HDRKSK-VLDRLNDADAKRYSCPTPRNSVNTREELKLANVVFPRC 58
Db 215 LYKPTWQLGKAFYGRKSKVVDLNLLEEVRLYSCPTPRNSVNTREELKRTDTIFWPGC 274
Qy 59 LLVRCGCGCGGTNNWRSCTNSGKTVKHYEVLPQEPGHKRRGRKTMALVDIQLDH 118
Db 275 LLVRCGCGNACCLHNCNECQVPRKVKYHEVLQLRP---KTGVRGLHKS LTDVALEH 331
Qy 119 HERCDCIC 126
Db 332 HEEDCVC 339
RESULT 7
Q9EQX6
ID Q9EQX6 PRELIMINARY; PRT; 345 AA.
AC Q9EQX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SPINAL CORD-DERIVED GROWTH FACTOR.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=KIDNEY;
RA Hanada T., Uti-tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDF/PDGF-C/follotein";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
DR EMBL; AB033830; BAB19969.1; -.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;
Query Match 43.8%; Score 322.5; DB 11; Length 345;
Best Local Similarity 50.0%; Pred. No. 5.4e-28;
Matches 64; Conservative 21; Mismatches 38; Indels 5; Gaps 4;
Qy 1 MYLDTPRYGRSY-HDRKSK-VLDRLNDADAKRYSCPTPRNSVNTREELKLANVVFPRC 58
Db 215 LYKPTWQLGKAFYGRKSKAVVDLNLLEEVRLYSCPTPRNSVNTREELKRTDTIFWPGC 274
Qy 59 LLVRCGCGCGGTNNWRSCTNSGKTVKHYEVLPQEPGHKRRGRKTMALVDIQLDH 118
Db 275 LLVRCGCGNACCLHNCNECQVPRKVKYHEVLQLRP-KIGVKGLHK--SLTDVALEH 331
Qy 119 HERCDCIC 126
Db 332 HEEDCVC 339
RESULT 8
Q9JHV8
ID Q9JHV8 PRELIMINARY; PRT; 345 AA.

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AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSER/NIH;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: Dynamic expression in embryonic tissues during
organogenesis.";
RL Mech. Dev. 0:0-0(2000);
DR EMBL; AF286725; AAF91483.1; -.
DR InterPro; IPR000072; -.
DR InterPro; IPR000859; -.
DR Pfam; PF00431; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00042; CUB; 1.
SQ SEQUENCE 345 AA; 3886 MW; FA1486BED6D362F8 CRC64;

Query Match 42.9%; Score 316.5; DB 11; Length 345;
Best Local Similarity 48.4%; Pred. No. 2.5e-27;
Matches 62; Conservative 21; Mismatches 40; Indels 5; Gaps 3;

QY . 1 MYLTPRYGRSY-HDRKSK-VDLRLNDDAKRYCTPRNYSVINREELKLANVFFPRC 58
: | : : : : : | : : : | : : | : : | : : | : : | : : | : : |
Db 215 LYKPTWLLGKAFLYKSKVNLNLLKEVKLYSCTPRNFSVSIRELKRTDTRFWPGC 274

QY 59 LLYVRCGGNGCGTVNRSCNSGKTVKYYHEVLQFEPGCHIKRGRKTMALVDIQLDH 118
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 275 LLYKRCGGNACCLHNCNECQVPRKVKYYHEVLQRP---RTGVKGLHKSLTDVALEH 331

QY 119 HERCDIC 126
| | | | |
Db 332 HEBCDCVC 339

RESULT 9
Q35251
ID Q35251 PRELIMINARY; PRT; 326 AA.
AC Q35251;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR D.
GN VEGF-D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
VEGF-D.";
RL Genomics 42:483-488(1997).
DR EMBL; AF014827; AAB66557.1; -.
DR HSSP; P15692; LVPP.
DR InterPro; IPR000072; -.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.

Query Match 14.5%; Score 107; DB 11; Length 326;
Best Local Similarity 27.8%; Pred. No. 0.00055;
Matches 35; Conservative 17; Mismatches 46; Indels 28; Gaps 6;

SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

QY 7 RYRGRSVHDKRSKVDLRLNDDAKRYCTPRNYSVINREEL-KLANVFFPRCLLVQRCG 65
: | : : : : : | : | : | : | : | : | : | : | : | : |
Db 93 RFAATFYDTLKV----IDEWQRTQCSPRETCVEVASELGKTTNTFFKPCVNVPRCG 148

QY 66 GNGCGGTVNRSCNSGKT---VKYHEV---LQFEPGCHIKRGRKTMALVDIQLDH 119
| | | | | | : | : | : | : | : | : | : | : | : |
Db 149 GCC-----NEESVMCMNTSTSYISKQLFEISVPLTSVP-----ELVPVKIANH 191

QY 120 ERCDIC 125
| | :
Db 192 TGCKCL 197

RESULT 10
Q43915
ID Q43915 PRELIMINARY; PRT; 354 AA.
AC Q43915;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GROWTH FACTOR FIGF.
GN FIGF OR VEGF-D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98140120; PubMed=9479493;
RA Rocchigiani M., Lestingi M., Luddi A., Orlandini M., Franco B.,
RA Rossi E., Ballabio A., Zuffardi O., Oliviero S.;
RT "Human FIGF: cloning, gene structure, and mapping to chromosome Xp22.1
between the FIGA and the GRPR genes.";
RL Genomics 47:207-216(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Yamada Y., Nezu J., Shimane M., Hirata Y.;
RT "Molecular cloning of a novel vascular endothelial growth factor,
VEGF-D.";
RL Genomics 42:483-488(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=98118549; PubMed=9435229;
RA Achen M.G., Jeltsch M., Kukk E., Maekinen T., Vitalli A., Wilks A.F.,
RA Alitalo K., Stacker S.A.;
RT "Vascular endothelial growth factor D (VEGF-D) is a ligand for the
tyrosine kinases VEGF receptor 2 (Flk1) and VEGF receptor 3 (Flt4).";
RL Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).
DR EMBL; Y12864; CAA73371.1; -.
DR EMBL; Y12865; CAA73371.1; JOINED.
DR EMBL; Y12866; CAA73371.1; JOINED.
DR EMBL; Y12867; CAA73371.1; JOINED.
DR EMBL; Y12868; CAA73371.1; JOINED.
DR EMBL; Y12869; CAA73371.1; JOINED.
DR EMBL; Y12870; CAA73371.1; JOINED.
DR EMBL; D89630; BAA24264.1; -.
DR EMBL; AJ000185; CAA03942.1; -.
DR EMBL; Y12863; CAA73370.1; -.
DR HSSP; P15692; LVPP.
DR InterPro; IPR000072; -.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
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Db	149	GCC-----NEEGVCMNTSTSYISKOLFELSVLTSP-----ELVPVKIANH 191
QY	120	ERCDCI 125
Db	192	TCCKCL 197
RESULT 12		
O54881	PRELIMINARY; PRT; 150 AA.	
ID	O54881	
AC	O54881;	
DT	01-JUN-1998 (TrEMBLrel. 06, Created)	
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B (FRAGMENT).	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=HEART;	
RL	Weill J., Eschenhagen T., Mittmann C., Scholz H.;	
RA	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF022952; AAB95447.1; -	
DR	HSSP; P15692; 1VPP.	
DR	InterPro; IPR000072; -	
DR	Pfam; PF00341; PDGF_1;	
DR	PROSITE; PS00249; PDGF_1; 1.	
DR	PROSITE; PS0278; PDGF_2; 1.	
DR	SMART; SM00141; PDGF; 1.	
FT	NON_TER 1	
FT	NON_TER 150	
FT	NON_TER 150	
SEQ	SEQUENCE 150 AA; 17243 MW; E2AC5CA9AD942F6A CRC64;	
Query Match 13.2%; Score 97.5; DB 11; Length 150;		
Best Local Similarity 28.8%; Pred. No. 0.0029;		
Matches 30; Conservative 15; Mismatches 38; Indels 21; Gaps		
QY	31	RYSCPTPRNYSNVIREUKLANV--FPFRCLLVRCGGCGCTVNRSCCTCNSGKTVKK 88
Db	13	RATCQPREVVVPLSMFEF-MGNVVKQFVPSCVTVQRCG---GCCPDGGLGCVPIGHQVRM 68
QY	89	YHEVLQFEGHKKRGRKTMALVDIOLDHHERCDICSSRP 132
Db	69	QILMIOY-----PSSQLGEMSLSEHSQCE-----RPKR 97
RESULT 13		
O9N413	PRELIMINARY; PRT; 304 AA.	
ID	O9N413	
AC	O9N413;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	Y39A3CL.6 PROTEIN.	
GN	Y39A3CL.6.	
OC	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BRISTOL N2;	
RA	MEDLINE=99069613; PubMed=9851916;	
RX	None;	
RT	"Genome sequence of the nematode C. elegans: a platform for	
RT	investigating biology. The C. elegans Sequencing Consortium.;"	
RL	Science 282:2012-2018(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	

RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024763; RAF60517.1; -
DR InterPro; IPR000072; -
DR InterPro; IPR001839; -
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00250; TGF BETA; UNKNOWN_1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 304 AA; 34131 MW; FB55120F513634D5 CRC64;

Query Match 13.2%; Score 97; DB 5; Length 304;
Best Local Similarity 26.9%; Pred. No. 0.0067;
Matches 32; Conservative 21; Mismatches 48; Indels 18; Gaps 6;

QY 17 KSKVDLRLNDADAKRYSCTPRNSVNIRELKLANVVFPRCLLVORCGNGCGGVNWR 76
DB 102 QSMKDKQGN-----TCNLQSVCPVPIQLSDPPQVLMYPKCYEVKQCVGSC-CNSVE-- 153
QY 77 SCTNSG--KTVKKYHEVLQFEGPHIKRRGRKTMALVDIQLDHERCDDCI-CSSRPPR 132
DB 154 --TCHPGTINLYKKHVAELLY-----IGNGRFNFMTKETMEHTSCSCFDCGSGNTPO 205

RESULT 14
Q64290
ID Q64290 PRELIMINARY; PRT; 207 AA.
AC Q64290;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN (VASCULAR
DE ENDOTHELIAL GROWTH FACTOR B 186).
GN VEGFB OR VRF OR VEGF-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=HEART;
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chilov D., Alitalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RL J. Biol. Chem. 271:19310-19317(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE BRAIN;
RX MEDLINE=96183052; PubMed=8607868;
RA Townson S., Lagercrantz J., Grimmond S., Silins G., Nordenskjold M.,
RA Weber G., Hayward N.K.;
RT "Characterization of the murine VEGF-related factor gene.";
RL Biochem. Biophys. Res. Commun. 220:922-928(1996).
DR EMBL; U52820; AAC52823.1; -
DR EMBL; U43836; AAC52932.1; -
DR HSP; P15692; IVPP.
DR MGD; MGI:106199; Vegfb.
DR InterPro; IPR000072; -
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.

DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
SQ SEQUENCE 207 AA; 21914 MW; 4817A5B96F6960C2 CRC64;

Query Match 13.0%; Score 95.5; DB 11; Length 207;
Best Local Similarity 27.9%; Pred. No. 0.0066;
Matches 29; Conservative 16; Mismatches 38; Indels 21; Gaps 5;

QY 31 RYSCTPRNSVNIRELKLANVVFPRCLLVORCGNGCGGVNWRSTCNSGKTGK 88
DB 44 RATCPQREVVVPLSMEL-MGNVVKQLVPSCVTVORCG---GCCPDDGLECVPTGQHV 99
QY 89 YHEVLQFEGPHIKRRGRKTMALVDIQLDHERCDDCISSRPPR 132
DB 100 QILMIQY-----PSSQLGEMSLSEHSQCEC-----RPAK 128

RESULT 15
O57352
ID O57352 PRELIMINARY; PRT; 418 AA.
AC O57352;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR.
GN VEGF-C.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98167900; PubMed=9435294;
RA Eichmann A., Corbel C., Jaifredo T., Breant V., Joukov V., Kumar V.,
RA Alitalo K., Le Douarin N.M.;
RT "Avian VEGF-C: cloning, embryonic expression pattern and stimulation
RT of the differentiation of VEGFR2-expressing endothelial cell
RT precursors.";
RL Development 125:743-752(1998).
DR EMBL; Y15837; CAA75799.1; -
DR HSP; P15692; IVPP.
DR InterPro; IPR000072; -
DR InterPro; IPR002400; -
DR Pfam; PF00341; PDGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD001629; -; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR SMART; SM00141; PDGF; 1.
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 111 418 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
SQ SEQUENCE 418 AA; 46839 MW; 099BFCC79151BF2B CRC64;

Query Match 12.1%; Score 89; DB 13; Length 418;
Best Local Similarity 18.0%; Pred. No. 0.072;
Matches 33; Conservative 20; Mismatches 56; Indels 74; Gaps 7;

QY 22 LDRLNDADAKRYSCTPRNSVNIREL-KLANVVFPRCLLVORCGNGC-----CGTV-- 73
DB 118 LKSIDFWRKTCQMPREVCVDVKGKFGATTNTFFKPCVSIYRCGCCNSEGQCNIST 177
QY 74 -----NWISCTNSKTV-KKYHEVLQ----- 94
DB 178 NYISKTLFEITVPLSHGPKPTVTSFANHTSCRCMSKLDVYRQVHSIRRLSLPATQCHV 237
QY 95 ----PEPGHKRRGRKTMALVDIQLDHH-----ERDCICSS- 128
DB 238 ANKTCPKNVNWNQICRCLAQHDFFGFSHLGDSDTSEGHICGPNKELDEETCCQCKG 297

Qy 129 -RP 130
||
Db 298 VRP 300

Search completed: September 26, 2001, 15:17:06
Job time: 117 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2001, 15:15:09 ; Search time 21.33 Seconds
(without alignments)
375,170 Million cell updates/sec

Title: US-09-662-783-4
Perfect score: 737
Sequence: 1 MYLTPYRGRSHYDRKSKV.....DIQLDHERCDCICSSRPPR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_0601.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
5 - 1	737	100.0	322	21	AAV71129 Human Platelet Der
5 - 2	737	100.0	370	21	AA848653 Human growth facto
5 - 3	737	100.0	370	21	AAV96864 SEQ. ID. 37 from W
5 - 4	737	100.0	370	21	AAV71130 Human Platelet Der
5 - 5	737	100.0	370	22	AA860888 Human VEGF-G prote
5 - 6	713	96.7	200	21	AAV71128 Human Platelet Der
5 - 7	686	93.1	370	21	AA848663 Mouse growth facto
5 - 8	681	92.4	370	22	AA860895 Human VEGF-G prote
5 - 9	380	51.6	66	21	AAV71132 Human Platelet Der
5 - 10	330	44.8	374	21	AA810639 Human VEGF-X prote
5 - 11	328.5	44.6	149	21	AA810642 Human VEGF-X PDGF-

12	328.5	44.6	318	21	AAV84558 A fragment of plat
13	328.5	44.6	339	21	AA858438 Lung cancer associ
14	328.5	44.6	345	20	AAV33679 Human VEGF-E prote
15	328.5	44.6	345	20	AAV41766 Human PRO200 prote
16	328.5	44.6	345	20	AAV30023 Human vascular end
17	328.5	44.6	345	21	AA848657 Human zvegfg3, SEQ
18	328.5	44.6	345	21	AA824250 Human platelet-der
19	328.5	44.6	345	21	AA844322 Human PRO200 (UNQ1
20	328.5	44.6	345	21	AA810633 Human RAGE generat
21	328.5	44.6	345	21	AA810634 Human VEGF-X homol
22	328.5	44.6	345	21	AA810635 Human VEGF-X prote
23	328.5	44.6	345	21	AA810636 Human VEGF-X prote
24	328.5	44.6	345	21	AA810644 Human VEGF-X prote
25	328.5	44.6	345	21	AA810650 Human 990126vegxp
26	328.5	44.6	345	21	AA810651 Human VEGF-X prote
27	328.5	44.6	345	21	AA819578 Human PRO200 (vasc
28	328.5	44.6	345	21	AA833414 Human PRO713 prote
29	328.5	44.6	345	21	AA824412 Human TANGO 128.
30	328.5	44.6	345	21	AA801419 Human growth facto
31	328.5	44.6	345	21	AA803003 Human growth facto
32	328.5	44.6	345	21	AAV96858 Amino acid sequenc
33	328.5	44.6	345	21	AAV84557 Bone morphogenic p
34	328.5	44.6	345	21	AAV59285 Human PRO200 prote
35	328.5	44.6	345	22	AA850980 Human PRO200 prote
36	328.5	44.6	345	22	AA849895 Human PRO200 prote
37	328.5	44.6	345	22	AA853074 Human angiogenesis
38	324.5	44.0	345	21	AA848658 Mouse zvegfg3, SEQ
39	324.5	44.0	345	21	AAV96861 Murine vascular en
40	324.5	44.0	345	21	AAV84559 A murine platelet-
41	318.5	43.2	354	21	AA810640 Human VEGF-X prote
42	318.5	43.2	354	21	AA810641 Human VEGF-X prote
43	308.5	41.9	113	21	AA810631 Human VEGF-X prote
44	308.5	41.9	113	21	AA810632 Human VEGF-X prote
45	292	39.6	227	21	AA810637 Human VEGF-X prote

ALIGNMENTS

RESULT 1
AAV71129
ID AAV71129 standard; peptide; 322 AA.
XX
AC AAV71129;
XX
XX
DT 08-SEP-2000 (first entry)
XX
DE Human Platelet Derived Growth Factor (PDGF)-D partial polypeptide #2.
XX
KW Platelet Derived Growth Factor-D; PDGF-D; human; cytostatic; vulnerary;
KW VEGF-G; Vascular Endothelial Growth Factor; antiatherosclerotic; tumour;
KW proliferative; activator; proliferation; differentiation; motility;
KW growth; PDGF-D receptor; antagonist; tissue remodelling; treat;
KW atherosclerosis; wound; metastasis.
OS Homo sapiens.
XX
XX W0200027879-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US26462.
XX
PR 10-NOV-1998; 98US-0107852.
PR 28-DEC-1998; 98US-0113997.
PR 28-AUG-1999; 99US-0150604.
PR 04-OCT-1999; 99US-0157108.
PR 05-OCT-1999; 99US-0157756.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Eriksson U, Aase K, Ponten A, Lee X, Uutela M, Alitalo K;


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VERSION    AA488780.1 GI:2218382
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SOURCE     human.
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 360)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CEBR). CDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
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US-09-662-783-4 x AA488780
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1 AATGTGCTGTGGAACTGCTCACTGGAGGCTCTGCATGCAATCAGG 50
83 ylysthrVallysthrHisGluValLeuGlnPheGluProGlyHis1 100
51 GAAACCCGTGAAAGATATCATGAGTATTACAGTTTGAGCTGCGCCACA 100
100 leLysArgArgGlyArgAlaLysThrMetAlaLeuValAspIleGlnLeu 116

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151 GATCACCATGAACGATGTGATTGCTATCTGCGAGCTCAAGACCACTCGA 198
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ACCESSION  BF021679
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SOURCE     house mouse.
ORGANISM   Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 523)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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MGI:1423777
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High quality sequence stop: 452.
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                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
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US-09-662-783-4 x BF021679
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131 CTCACAGCAACATGCGAGCTTTGGCAAGCGCTTCCTGCTGATGGAA 180
16 glySerLys...ValAspLeuAspArgLeuAsnAspAlaLysArgT 32
181 AAAAGCAAGTGGTGAATCTGAATCTCTCTAAAGGAAGAGGTAAACTCT 230

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